

					GenCore version 5.1.6
Copyright (c) 1993 - 2003	Compugen Ltd.				
OM protein - protein search, using sw model					
Run on:	July 9, 2003, 12:40:38 ;	Search time:	35 Seconds		
Sequence:	MAJLCFVLLCGVADLRLSL.....AVIGVVLALVNLGLIFCCR	(without alignment)	966.067 Million cell updates/sec		
Scoring table:	BLOSUM62				
	Gapop 10.0 , Gapext 0.5				
Searched:	908470 seqs, 133250520 residues				
Total number of hits satisfying chosen parameters:	908470				
Minimum DB seq length:	0				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
Database :	Listing first 45 summaries				
A_Geneseq_101002:*					
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21: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2001.DAT:*					
22: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2002.DAT:*					
23: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2002.DAT:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description	
1	1238	91.1	352	22 AAY72878	Human PRO5723 protein
2	1238	91.1	352	22 AAB65294	Human PRO5723 protein
3	1238	91.1	352	22 AAB50930	Human PRO5723 protein
4	1238	91.1	352	23 ABB95562	Human androgenesis
5	1238	91.1	352	23 ABB84556	Human PRO5723 protein
6	1238	91.1	365	19 AAW69697	Human coxsackievirus
7	1238	91.1	365	19 AAW57212	Human coxsackievirus
8	1238	91.1	365	22 AAB47477	Human CAR protein
9	1238	91.1	365	23 ABB0840	Human coxsackievirus
10	1216	89.5	352	19 AAW69698	Mouse coxsackievirus
ALIGNMENTS					
RESULT 1					
ID AAY72878					
AAV72878 standard; Protein; 352 AA.					
XX					
AC AAY72878;					
XX					
DT 31-MAY-2001 (first entry)					
XX					
DE Human PRO5723 protein encoded by DNA82361 cDNA clone.					
XX					
HH Human; PRO5723; antiinflammatory; dermatological; immunosuppressive; anti-rheumatic; antiarthritic; osteopathic; antihaemolytic; antiallergic; anti-thyroid; antidiabetic; antiviral; antisporotrichosis; antiasthmatic; inhibitor; therapy; systemic lupus erythematosus; spordyloarthropathy; systemic sclerosis; systemic vasculitis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; autoimmune thrombocytopenia; Guillain-Barre syndrome; Whipple's disease; demyelinating polyneuropathy; primary biliary cirrhosis; sclerosing cholangitis; hepatobiliary disease; primary glomerulonephritis; skin disease; inflammatory bowel disease; gluten-sensitive enteropathy; skin disease; allergic rhinitis; atop dermatitis; food hypersensitivity; urticaria; eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection; idiopathic pulmonary fibrosis; graft-versus-host-disease.					
OS Homo sapiens.					
PH Key Peptide					
PT Location/Qualifiers 1..19					
FT Protein 20..352					
FT /label= Signal_peptide					
FT Modified-site 31..38					
FT /label= Tyrosine_kinase_phosphorylation_site					

FT Modified-site 78..84
 FT /label= Tyrosine_kinase_phosphorylation_site
 FT 96..125
 FT Region /label= Myelin_P0_protein
 FT 106..109
 FT Domain /label= Immunoglobulin_domain
 FT 155..214
 FT /note= "Asn is N-glycosylated"
 FT 201..204
 FT /note= "Asn is N-glycosylated"
 FT Region /label= Tyrosine_kinase_phosphorylation_site
 FT 229..301
 FT /label= Myelin_P0_protein
 FT 231..256
 FT /label= Transmembrane_domain
 FT 262..269
 FT /label= Tyrosine_kinase_phosphorylation_site
 FT note= "Asn is N-glycosylated"
 XX WO200116319-A2.
 PN XX
 XX PD 08-MAR-2001.
 XX PR 23-AUG-2000; 2000WO-US23522.
 PR XX
 PR 31-AUG-1999; 99US-0151733.
 PR 01-SEP-1999; 99WO-US20111.
 PR 16-DEC-1999; 99WO-US30095.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 05-JUN-2000; 2000WO-US209832.
 PA XX
 -XX (GBTB) GENENTECH INC.
 PT Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;
 PI Watanabe CK, Wood WI;
 XX WPI; 2001-226690/23.
 DR N-PSDB; AAD02924.
 XX
 PT New PRO polypeptides for treating immune related and inflammatory
 diseases such as rheumatoid arthritis, systemic vasculitis, asthma,
 autoimmune hemolytic anemia, and diabetes mellitus
 XX
 PS Claim 10; Fig 10; 118pp; English.
 XX
 CC The present sequence is PRO5723 protein encoded by DNA82361 cDNA
 CC clone. PRO protein, its agonist or antagonist or its antibody which are
 CC capable of enhancing or inhibiting the proliferation of T-lymphocytes
 CC or of increasing the infiltration of inflammatory cells into a tissue
 CC are useful in the diagnosis and treatment of immune-related diseases
 CC in mammals. The PRO protein is useful for treating systemic lupus
 CC erythematosis, rheumatoid arthritis, osteoarthritis, Juvenile chronic
 CC arthritis, spondyloarthropathy, systemic sclerosis, idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, systemic sclerosis,
 CC thyroïditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinating disease of the central or peripheral nervous system,
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC chronic inflammatory demyelinating polyneuropathy, hepatobilary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, autoimmune or immune-mediated skin diseases such as bullous
 CC skin disease, erythema multiforme and contact dermatitis, psoriasis,
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity and urticaria, immunologic diseases of the lung,
 CC such as eosinophilic pneumonia, idiopathic pulmonary fibrosis, hyper-
 CC sensitivity pneumonitis, transplantation associated diseases such as
 CC graft rejection or graft-versus-host-disease.
 XX graft rejection or graft-versus-host-disease.
 SQ Sequence 352 AA;
 SQ Query Match 91.1%; Score 1238; DB 22; Length 352;
 SQ Best Local Similarity 89.3%; Pred. No. 2..4e-108;
 SQ Matches 233; Conservative 13; Mismatches 15; Index 0; Gaps 0;
 QY 1 MAUUCFVLLCGVADLRTSLSTTPPEQWIEKAKGETAYLPCTPFTLGSDQGLDIEWILS 60
 Db 1 MAUUCFVLLCGVUDFARSLSITPPEQWIEKAKGETAYLPCKFTLSPEDOGDLIEWILS 60
 QY 121 KVKKAPSGVGNKKIQLTLLKSGSGTRCYVDGSEBIGHDKLKEPKGSPLIYEWQLSN 180
 Db 121 KVKKAPSGVGNKKIQLTLLKSGSGTRCYVDGSEBIGHDKLKEPKGSPLIYEWQLSN 180
 QY 181 SOKLQPTWLAEMTSPTVSKVNASTEYSGTYACTVVKQNGSPDCLRLDVVPSPNRAGTIA 240
 Db 181 SOKMPTSWLAEMTSSVSKVNASEISGTYSCTVRNKGSDOCLRLNVVPPSNKAGLIA 240
 QY 241 GAVIGVIALVALVIGLIFCCR 261
 Db 241 GAIIGTULALALIGLIFCCR 261
 RESULT 2
 ID AAB65294
 ID AAB65294 standard; Protein; 352 AA.
 XX
 AC AAB65294;
 XX DT 02-APR-2001 (first entry)
 XX
 DE Human PRO5723 protein sequence SEQ ID NO:505.
 KW Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO20073454-A1.
 XX PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US1252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143448.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US2313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US0019.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04741.
 PR 22-FEB-2000; 2000WO-US0414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 Grimaldi CJ, Gurney AL, Klagsbald IJ, Napier MA, Pan J, Paoni NF,
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 Zhang Z;
 XX DR WPI; 2001-032160/04.
 XX DR N-PSDB; AAC44263.
 XX PT PRO polynucleotides used to produce polypeptides used to target
 bioactive molecules such as toxins, radiolabels or antibodies, to
 specific cells, to cause targeted cell death -
 XX PS Claim 12; Fig 31B; 935pp; English.
 XX The present invention describes human secreted and transmembrane PRO
 proteins. The PRO proteins have cytostatic activity. The PRO proteins
 can be used for targeted delivery of bioactive molecules, such as
 toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 sequences, and their fragments, can be used as hybridization probes, in
 chromosomal and gene mapping, and in the generation of anti-sense RNA
 and DNA. They may also be used to produce transgenic animals which are
 used to develop and screen therapeutically useful reagents. The PRO
 nucleotide and protein sequence can be used for tissue typing and in
 treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 AAC44270 to AAC4470 represent PCR primers and hybridization probes used
 in the isolation of human PRO sequences. AAC44087 to AAC4429 and
 AAC65154 to AAB5300 represent human PRO polynucleotide and protein
 sequences given in the exemplification of the present invention.
 XX SQ Sequence 352 AA;

Query Match 91.1%; Score 1238; DB 22; Length 352;
 Best Local Similarity 89.3%; P-Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy	1	MALLCIVULLGGVADLTLRSLLTPEOMIEKAKGETAYLPRTFTLGEDQGDLDIWLIS	60
Db	1	MALLCIVULLGGVADLTLRSLLTPEOMIEKAKGETAYLPRTFTLGEDQGDLDIWLIS	60
Qy	61	PADNQKDQVILLYSGKRYDDYQDLKGGRVFTSNDLKSASINTNLQSLDGYQC	120
Db	61	PADNQKDQVILLYSGKRYDDYQDLKGGRVFTSNDLKSASINTNLQSLDGYQC	120
Qy	121	KYKKAPEGVGNKKQLTVLKPSCTRCYVGSEBIGNPFLKCEPKEGSLPLVYEWQKLSN	180
Db	121	KYKKAPEGVGNKKQLTVLKPSCTRCYVGSEBIGNPFLKCEPKEGSLPLVYEWQKLSN	180
Qy	181	SQKPTLWALEMSPVTSVKNASTEYKGTYCTVKNRVSQCLRLDVWVPPSNRACTIA	240
Db	181	SQKPTLWALEMSPVTSVKNASTEYKGTYCTVKNRVSQCLRLDVWVPPSNACTIA	240
Qy	241	GAVIGVIALVVLVGLIFCCR 261	
Db	241	GAVIGVIALVVLVGLIFCCR 261	

RESULT 3
 ARB5030 standard; Protein; 352 AA.
 AC AAB5030;
 XX AAB5030;
 ID AAB5030 standard; Protein; 352 AA.
 DT 21-MAR-2001 (first entry)
 XX Human PRO5723 protein.
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;

KW antirheumatic; cardiotonic; antianaemic; immunosuppressive; antithyroid;
 KW antiidiabetic; noctropic; neuroprotective; hepatotropic; virucide;
 KW antiallergic; antiasthmatic; immune related disorder;
 KW hepatobiliary disease; autoimmune disease; allergy.
 XX OS Homo sapiens.
 XX PN WO200173452-A2.
 XX PD 07-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-US15264.
 XX PR 02-JUN-1999; 99WO-US12252.
 PR 20-JUN-1999; 99US-0144732.
 PR 20-JUN-1999; 99US-0144758.
 PR 28-JUN-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US2011.
 PR 15-SEP-1999; 99WO-US21090.
 PR 29-OCT-1999; 99US-016286.
 PR 30-NOV-1999; 99WO-US2813.
 PR 01-DEC-1999; 99WO-US28634.
 PR 09-DEC-1999; 99US-0170862.
 PR 20-DEC-1999; 99WO-US30311.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04144.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 15-MAR-2000; 2000WO-US06844.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 XX PA (GETH) GENENTECH INC.
 XX PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,
 Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
 PR Wood WI;
 XX DR WPI; 2001-025253/03.
 XX DR N-PSDB; AAC91489.
 XX PT Thirty three nucleic acids encoding PRO polypeptides which are useful
 in the diagnosis and treatment of immune related disorders, e.g.
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 PT thyroiditis and diabetes mellitus -
 XX PS Claim 58; Fig 58; 218pp; English.
 XX The present sequence is one of thirty three novel PRO polypeptides.
 CC The PRO polypeptides, anti-PRO antibodies, agonists and
 CC antagonists are useful for treating and diagnosing immune related
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjögren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 CC immun-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
 CC (such as infectious, autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC food hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.

Sequence 352 AA;

Query Match 91.1%; Score 1238; DB 22; length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108; Length 352;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 Ov 1 MAUICCFVLLCGVADLTSLSITTPPEQMEKAKGETAYLPCKFTLSPEDQGLDIEWLS 60
 1 MAUICCFVLLCGVADLTSLSITTPPEQMEKAKGETAYLPCKFTLSPEDQGLDIEWLS 60
 Db 61 PADNQKDQVILYSGKIDYYQDKGRVHTSNDLKSGSASINTNLQSDIGTYQC 120
 Qy 61 PADNQKDQVILYSGKIDYYQDKGRVHTSNDLKSGSASINTNLQSDIGTYQC 120
 Db 61 PADNQKDQVILYSGKIDYYQDKGRVHTSNDLKSGSASINTNLQSDIGTYQC 120
 Qy 121 KVKKAPGYNKKIQLTVLKKPSGTRCYVDGSEERIGNDKLKKEPKESGLPLLYEWKLQN 180
 121 KVKKAPGYNKKIQLTVLKKPSGTRCYVDGSEERIGNDKLKKEPKESGLPLLYEWKLQN 180
 Db 181 SOKLPTLMLEMSPVUTSVKNASTEYSGTYSCTVKNRVGSQDCLRLDVPPRNACTIA 240
 181 SOKMPTSMLEMSPVUTSVKNASTEYSGTYSCTVKNRVGSQDCLRLDVPPRNACTIA 240
 Qy 241 GAVIGVIALWLIGLICCR 261
 241 GAVIGVIALWLIGLICCR 261

RESULT 4
 ABB95562
 ID ABB95562 standard; Protein; 352 AA.
 AC ABB95562;
 XX DT 19-JUL-2002 (first entry)
 XX DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
 XX KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cytostatic; antiangiogenic; hypotensive; pulmonary;
 KW antiarteriosclerotic.
 OS Homo sapiens.
 XX PN WO200208284-A2.
 XX PD 31-JAN-2002.
 XX PT 09-JUL-2001; 2001WO-US21735.
 PR 17-AUG-2000; 2000US-0543657.
 PR 23-AUG-2000; 2000WO-US2352.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-220978P.
 PR 15-SEP-2000; 2000US-00000P.
 PR 18-SEP-2000; 2000US-0564610.
 PR 18-SEP-2000; 2000US-0565350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 03-NOV-2000; 2000US-0709238.
 PR 03-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US31956.
 PR 22-JAN-2001; 2001US-076769.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06566.
 PR 09-MAR-2001; 2001US-0802406.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854288.
 PR 25-MAY-2001; 2001US-0866038.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870554.
 PR 01-JUN-2001; 2001WO-US17433.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX PA (GETH-) GENENTECH INC.
 PA (BAKE-) BAKER K P.
 PA (FERR-) FERRARA N.
 PA (GERR-) GERRITSEN M E.
 PA (GODD-) GODDARD A.
 PA (GODO-) GODOWSKI P J.
 PA (GURN-) GURNEY A L.
 PA (HILL-) HILLIAN K J.
 PA (MARS-) MARSTERS S A.
 PA (PANJ-) PAN J.
 PA (PAON-) PAONI N P.
 PA (STEP-) STEPHAN J F.
 PA (WATA-) WATANABE C K.
 PA (WILL-) WILLIAMS P M.
 PA (WOOD-) WOOD W I.
 XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillian KJ, Marsters SA, Pan J, Paoni NP; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W.
 XX DR WPI; 2002-171993/22.
 XX PT N-PSDB; ABL95700.
 XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 XX PT Claim 11; Fig 280; 567pp; English.
 XX CC The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
 XX SQ Sequence 352 AA;
 Query Match 91.1%; Score 1238; DB 23; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108; Length 352;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 Ov 1 MAUICCFVLLCGVADLTSLSITTPPEQMEKAKGETAYLPCKFTLSPEDQGLDIEWLS 60
 1 MAUICCFVLLCGVADLTSLSITTPPEQMEKAKGETAYLPCKFTLSPEDQGLDIEWLS 60
 Db 61 PADNQKDQVILYSGKIDYYQDKGRVHTSNDLKSGSASINTNLQSDIGTYQC 120
 Qy 61 PADNQKDQVILYSGKIDYYQDKGRVHTSNDLKSGSASINTNLQSDIGTYQC 120
 Db 61 PADNQKDQVILYSGKIDYYQDKGRVHTSNDLKSGSASINTNLQSDIGTYQC 120

Qy 121 KVKKAPGUNKKIQLTVLKLPSGRCTYVUDGSEB1GNDFRKCEPKERSSLPLIYEWORKLSN 180
 PR 30-MAY-2001; 2001WO-US17433.
 Db 121 KVKKAPGUNKKIQLTVLKLPSGRCTYVUDGSEB1GNDFRKCEPKERSSLPLIYEWORKLSN 180
 XX (GETH) GENENTECH INC.
 Qy 181 SOKLPTMLAEMTSPVSVKNASTEYSCSYCTVKNRVSQDCLRLDVPPSNRAGTIA 240
 PR 181 SOKLPTMLAEMTSPVSVKNASTEYSCSYCTVKNRVSQDCLRLDVPPSNRAGTIA 240
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski RJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX DR WPI; 2002-090516/12.
 Db 241 GAVIGVULALVIGLIIFCCR 261
 PR N-PSDB; ABL88211.
 XX
 RESULT 5
 ABB84956 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 ID ABB84956 standard; Protein; 352 AA. PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 XX
 AC ABB84956; PS Claim 11; Fig 230; 565pp; English.
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO5723 protein sequence SEQ ID NO:280.
 XX
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
 KW Homo sapiens.
 OS
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 PR 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-042922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 10-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US330873.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-JAN-2001; 2001US-0767609.
 PR 26-FEB-2001; 2001US-0796498.
 PR 01-MAR-2001; 2001WO-US06520.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.

PR 30-MAY-2001; 2001WO-US17433.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski RJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX DR WPI; 2002-090516/12.
 XX
 CC ABL8872 to ABL88258 encode the PRO proteins given in ABL84817 to ABL88003. The PRO proteins and poly nucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO poly nucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal - e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO poly nucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.

XX
 Sequence 352 AA;

SQ Query Match Best Local Similarity 91.1%; Score 1238; DB 23; Length 352;
 Matches 233; Conservative 13; Mismatches 15; Pred. No. 2.4e-108; Index 0; Gaps 0;

Qy 1 MAUCLCFLCCVADUTRSLSITPPQMEKAGETTYLPCRFTGPEDQPLDTSWLS 60
 PR 1 MAUCLCFLCCVADUTRSLSITPPQMEKAGETTYLPCRFTGPEDQPLDTSWLS 60
 Db 61 PADNOKDQVILYSGKIVDPYDPLKGRVHTFSNDLKSQDASINVNTLQSLSDIGTYOC 120
 PR 61 PADNOKDQVILYSGKIVDPYDPLKGRVHTFSNDLKSQDASINVNTLQSLSDIGTYOC 120
 Qy 121 KVKKAPGUNKKIQLTVLKLPSGRCTYVUDGSEB1GNDFRKCEPKERSSLPLIYEWORKLSN 180
 PR 121 KVKKAPGUNKKIQLTVLKLPSGRCTYVUDGSEB1GNDFRKCEPKERSSLPLIYEWORKLSN 180
 Db 181 SOKLPTMLAEMTSPVSVKNASTEYSCSYCTVKNRVSQDCLRLDVPPSNRAGTIA 240
 PR 181 SOKLPTMLAEMTSPVSVKNASTEYSCSYCTVKNRVSQDCLRLDVPPSNRAGTIA 240
 Qy 241 GAVIGVULALVIGLIIFCCR 261
 PR 241 GAVIGVULALVIGLIIFCCR 261
 Db 241 GAVIGVULALVIGLIIFCCR 261

RESULT 6
 PR AAW69697
 ID AAW69697 standard; Protein; 365 AA.
 XX
 AC AAW69697;
 XX
 DT 07-DEC-1998 (first entry)
 XX
 DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
 XX
 HCAR: coxsackievirus receptor; CVB: adenovirus; Ad2 receptor;
 KW Ad5 receptor; human; infection; vaccine; therapy.

CC protein are useful for blocking CAR expression. Cell-free assays which include combining CAR protein and a candidate/test compound are useful in screening for drugs which interact with CAR protein.

XX SQ sequence 365 AA;

Query Match 91.1%; Score 1238; DB 19; Length 365;
Best Local Similarity 89.3%; Pred. No. 2 6e-108; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLCFLVLLCGVADLRSLSITPBMIEAKGETAYLPORFTLGPDQPLDIELWLS 60
1 MAUCLCFVLLCGVADLRSLSITPBMIEAKGETAYLPORFTLGPDQPLDIELWLS 60

Db 61 PADNQKDQVILYSGDKIIDDYQDLKGRVHTFSNDLKSGDASINTNLQSLDIGYQC 120
61 PADNQKDQVILYSGDKIIDDYQDLKGRVHTFSNDLKSGDASINTNLQSLDIGYQC 120

Db 61 GAIGITLALALIGLIFCCR 261
61 GAIGITLALALIGLIFCCR 261

QY 121 KVKKAPGNGNKKIQLTULKGSGTRCYDGSEREGNDFKLKCEPKPSLPLIYEWOKLSN 180
121 KVKKAPGNGNKKIQLTULKGSGTRCYDGSEREGNDFKLKCEPKPSLPLIYEWOKLSN 180

Db 181 SOKLPTLWLAEMTSPIVSVKRASTEYSGTISCTVKRGRVSDQCLRLDVPPSNRAGTIA 240
181 SOKMPTSWLAEMTSPIVSVKRASTEYSGTISCTVKRGRVSDQCLRLDVPPSNRAGTIA 240

QY 241 GAVIVGVLALVALVGLIIFCCR 261
241 GAVIVGVLALVALVGLIIFCCR 261

Db 241 GAIGITLALALIGLIFCCR 261
GAIGITLALALIGLIFCCR 261

RESULT 8

AB47270 ID AAB47270 standard; Protein: 365 AA.

AC AAB47270;
XX DT 06-AUG-2001 (first entry)
DE Human CAR.
XX KW Coxsackie virus and/or Adenovirus receptor; CAR; transgenic mouse; KW transgene; tCAR; transduction; integrin; gene transfer; lymphocyte; KW lymphocyte-specific transcription regulatory sequence; T cell.

OS Homo sapiens.

PH Key Protein PT Location/Qualifiers 1.262 /note= "Claimed tCAR"
XX US6245966-B1.
XX PD 12-JUN-2001.
XX PP 19-MAR-1999; 99US-0272496.
XX PR 14-JUL-1998; 98US-0092782.
XX PA (UYTE-) UNIV TECHNOLOGY CORP.
XX PI DeGregori J;
XX DR WPI; 2001366549/38.
XX N-PSDB; AMC85813.

PT Transgenic mouse comprising a nucleotide sequence encoding a truncated Coxsackie virus and/or Adenovirus receptor (tCAR) polypeptide useful for the analysis of cellular physiology -
PS Claim 3; Column 15-18; 21pp; English.

XX This sequence shows a Coxsackie virus and/or Adenovirus receptor (CAR).

CC polypeptide. The DNA encoding this sequence was used in the method of invention to produce a transgenic mouse whose genome comprises a transgene comprising a nucleotide sequence encoding a truncated CAR polypeptide (tCAR) operably linked to a lymphocyte-specific transcription regulatory nucleotide sequence. The tCAR is expressed in the lymphocytes of the mouse at levels sufficient for increased susceptibility to adenoviral transduction of the lymphocytes without affecting the expression of endogenous integrins in the lymphocytes. The transgenic mouse is useful for the analysis of pathways, via gene transfer, which control various aspects of cellular physiology either in vitro or in vivo. The tCAR-regulatory sequence construct facilitates either the in vivo delivery of genes into lymphoid organs or the ex vivo delivery of genes into transgenic T cells as T cells expressing the truncated form of tCAR are highly efficient target cells for adenoviral transduction.

CC Sequence 365 AA;

Query Match 91.1%; Score 1238; DB 22; Length 365;
Best Local Similarity 89.3%; Pred. No. 2 6e-108; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLCFLVLLCGVADLRSLSITPBMIEAKGETAYLPORFTLGPDQPLDIELWLS 60
1 MAUCLCFVLLCGVADLRSLSITPBMIEAKGETAYLPORFTLGPDQPLDIELWLS 60

Db 61 PADNQKDQVILYSGDKIIDDYQDLKGRVHTFSNDLKSGDASINTNLQSLDIGYQC 120
61 PADNQKDQVILYSGDKIIDDYQDLKGRVHTFSNDLKSGDASINTNLQSLDIGYQC 120

Db 61 GAIGITLALALIGLIFCCR 261
61 GAIGITLALALIGLIFCCR 261

QY 121 KVKKAPGNGNKKIQLTULKGSGTRCYDGSEREGNDFKLKCEPKPSLPLIYEWOKLSN 180
121 KVKKAPGNGNKKIQLTULKGSGTRCYDGSEREGNDFKLKCEPKPSLPLIYEWOKLSN 180

Db 181 SOKLPTLWLAEMTSPIVSVKRASTEYSGTISCTVKRGRVSDQCLRLDVPPSNRAGTIA 240
181 SOKMPTSWLAEMTSPIVSVKRASTEYSGTISCTVKRGRVSDQCLRLDVPPSNRAGTIA 240

QY 241 GAVIVGVLALVALVGLIIFCCR 261
241 GAVIVGVLALVALVGLIIFCCR 261

Db 241 GAIGITLALALIGLIFCCR 261
GAIGITLALALIGLIFCCR 261

RESULT 9

ABB08040 ID ABB08040 standard; Protein: 365 AA.

AC ABB08040;
XX PT Location/Qualifiers 1.262 /note= "Claimed tCAR"
XX US6245966-B1.
XX PD 12-JUN-2001.
XX PP 19-MAR-1999; 99US-0272496.
XX PR 14-JUL-1998; 98US-0092782.
XX PA (UYTE-) UNIV TECHNOLOGY CORP.
XX PI DeGregori J;
XX DR WPI; 2001366549/38.
XX N-PSDB; AMC85813.

PT Transgenic mouse comprising a nucleotide sequence encoding a truncated Coxsackie virus and/or Adenovirus receptor (tCAR) polypeptide useful for the analysis of cellular physiology -
PS Claim 3; Column 15-18; 21pp; English.

XX This sequence shows a Coxsackie virus and/or Adenovirus receptor (CAR).

CC polyptide. The DNA encoding this sequence was used in the method of invention to produce a transgenic mouse whose genome comprises a transgene comprising a nucleotide sequence encoding a truncated CAR polypeptide (tCAR) operably linked to a lymphocyte-specific transcription regulatory nucleotide sequence. The tCAR is expressed in the lymphocytes of the mouse at levels sufficient for increased susceptibility to adenoviral transduction of the lymphocytes without affecting the expression of endogenous integrins in the lymphocytes. The transgenic mouse is useful for the analysis of pathways, via gene transfer, which control various aspects of cellular physiology either in vitro or in vivo. The tCAR-regulatory sequence construct facilitates either the in vivo delivery of genes into lymphoid organs or the ex vivo delivery of genes into transgenic T cells as T cells expressing the truncated form of tCAR are highly efficient target cells for adenoviral transduction.

CC Sequence 365 AA;

Query Match 91.1%; Score 1238; DB 22; Length 365;
Best Local Similarity 89.3%; Pred. No. 2 6e-108; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLCFLVLLCGVADLRSLSITPBMIEAKGETAYLPORFTLGPDQPLDIELWLS 60
1 MAUCLCFVLLCGVADLRSLSITPBMIEAKGETAYLPORFTLGPDQPLDIELWLS 60

Db 61 PADNQKDQVILYSGDKIIDDYQDLKGRVHTFSNDLKSGDASINTNLQSLDIGYQC 120
61 PADNQKDQVILYSGDKIIDDYQDLKGRVHTFSNDLKSGDASINTNLQSLDIGYQC 120

Db 61 GAIGITLALALIGLIFCCR 261
61 GAIGITLALALIGLIFCCR 261

QY 121 KVKKAPGNGNKKIQLTULKGSGTRCYDGSEREGNDFKLKCEPKPSLPLIYEWOKLSN 180
121 KVKKAPGNGNKKIQLTULKGSGTRCYDGSEREGNDFKLKCEPKPSLPLIYEWOKLSN 180

Db 181 SOKLPTLWLAEMTSPIVSVKRASTEYSGTISCTVKRGRVSDQCLRLDVPPSNRAGTIA 240
181 SOKMPTSWLAEMTSPIVSVKRASTEYSGTISCTVKRGRVSDQCLRLDVPPSNRAGTIA 240

QY 241 GAVIVGVLALVALVGLIIFCCR 261
241 GAVIVGVLALVALVGLIIFCCR 261

Db 241 GAIGITLALALIGLIFCCR 261
GAIGITLALALIGLIFCCR 261

WPI, 2002-471317/50.

DR N-PSDB; AB160622.

A targeting molecule for use in forming complexes to treat cancer, such as adenocarcinoma of the prostate, comprises a soluble adenoviral receptor domain, a trimerisation domain and a targeting ligand domain -

Example 14; Page 47; 75pp; English.

The invention relates to a targeting molecule that comprises a soluble adenoviral receptor domain, a trimerisation domain and a targeting ligand particle to a cell expressing a cell surface molecule. The method involves contacting the adenoviral particle with the targeting molecule to form a complex, and contacting the cell with the complex, and in delivering a heterologous gene selectively to a cell. The complex is used for preparing a medicament for treatment of disease in a human mammal, such as cancer, preferably adenocarcinoma of the prostate, by gene therapy. The present sequence represents the human coxsackie-adenovirus receptor (CAR), a 46 kDa transmembrane protein. The soluble form of CAR (scAR) can be used in the targeting molecule of the invention.

SQ Sequence

PA

Query Match Best Local Similarity 91.1%; Score 1238; DB 23; Length 365;

Matches 233; Conservative 89.3%; Pred. No. 2.6e-108; Indels 0; Gaps 0;

QY 1 MALLCFCVLLGVALDRLRSLSITTPEMTEKAGETAYLPCKRPLTGPDQGDIDWILS DR N-PSDB; AAV50430.

Db 1 MALLCFCVLLGVALDRLRSLSITTPEMTEKAGETAYLPCKRPLTGPDQGDIDWILS 60

QY 61 PADNOKQDVQVILLYSGDKYDDYQDLKGCRVHFTSNDLKSQDASINTNLQLSDIGTYQC DR WO9833819-A1.

Db 61 PADNOKQDVQVILLYSGDKYDDYQDLKGCRVHFTSNDLKSQDASINTNLQLSDIGTYQC 120

QY 181 SOKUPTLWLAEMSPVSPVSKVNASTEYGTCTYKVNRVGSQDCLRLDVPPSNRAGTIA DR 06-AUG-1998.

Db 181 SOKUPTLWLAEMSPVSPVSKVNASTEYGTCTYKVNRVGSQDCLRLDVPPSNRAGTIA 120

QY 121 KVVKAPGYNKKIQLTVLKPSGRCPYDGEELGNDFLKLKCPEKEGSPLLPEWQQLSN DR 30-JAN-1997; 97US-0036986.

Db 121 KVVKAPGYNKKIQLTVLKPSGRCPYDGEELGNDFLKLKCPEKEGSPLLPEWQQLSN 180

QY 121 KVVKAPGYNKKIQLTVLKPSGRCPYDGEELGNDFLKLKCPEKEGSPLLPEWQQLSN DR 180

Db 181 SOKUPTLWLAEMSPVSPVSKVNASTEYGTCTYKVNRVGSQDCLRLDVPPSNRAGTIA 240

QY 241 GAVIVGLAALVLGLIIFCCR DR 30-JAN-1997; 97US-0036986.

Db 241 GAVIVGLAALVLGLIIFCCR 261

RESULT 10

AAW69698 ID AAW69698 standard; Protein; 352 AA.

AC AAW69698; XX

DT 07-DEC-1998 (first entry)

DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.

XX KW MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor; Ad5 receptor; mouse; infection; vaccine; therapy.

OS Mus sp.

FH Key Domain 35..130 Location/Qualifiers

FT /note= "extracellular immunoglobulin domain"

FT Domain 155..220 /note= "extracellular immunoglobulin domain"

FT Region 45..52 /note= "CVB binding region (Claim 6)"

FT Region 47..51 /note= "Ad2/5 and CVB binding region (Claim 6)"

/note= "Ad2/Ads binding region (Claim 6)"

FT Region 53..57 /note= "Ad2/Ads binding region (Claim 6)"

FT Region 69..73 /note= "Ad2/Ads binding region (Claim 6)"

FT Region 72..77 /note= "CVB-binding region (Claim 6)"

FT Region 77..79 /note= "Ad2/Ads binding region (Claim 6)"

FT Region 96..100 /note= "Ad2/5 and CVB binding region (Claim 6)"

FT Region 122..127 /note= "Ad2/5 and CVB binding region (Claim 6)"

FT Region 128..137 /note= "Ad2/5 and CVB binding region (Claim 6)"

FT Region 180 WO9833819-A1.

PR 06-AUG-1998.

XX 30-JAN-1998; 97US-0036986.

PR 30-JAN-1997; 97US-0036986.

XX PA (UYNY) UNTV NEW YORK STATE.

XX PI Philipson L, Tomko RP;

XX WI; 1998-437397/37.

XX DR N-PSDB; AAV50430.

XX PT DNA encoding human receptor for adenovirus C and coxsackievirus B -

PT for preventing and treating viral infection and rendering cells susceptible to transformation by adenoviral vectors in gene therapy

XX CC Claim 3; Page 70-71; 88pp; English.

This is the amino acid sequence of mouse MCAR, a protein that serves as a cellular receptor for adenoviruses of the serotypes 2 and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The sequence was deduced from an isolated cDNA clone for MCAR (see AAU50430). The invention also provides host cells transformed with DNA molecules encoding MCAR or human HCAR (see AAW69697), and methods of producing the recombinant proteins or their derivatives. These proteins, their extracellular domains, as well as oligopeptides (see AAW69699-708) which bind virus, are claimed. Isolated HCAR or MCAR proteins or their fragments or variants are used to prevent or treat virus infections and for inhibiting the infectivity of Ad2, Ad5 or CVB. Methods are also provided for detecting or measuring the quantity of HCAR or MCAR in a sample, and for identifying analytes capable of binding to HCAR or MCAR.

XX SQ Sequence 352 AA:

Query Match Best Local Similarity 89.5%; Score 1216; DB 19; Length 352;

Matches 229; Conservative 88.1%; Pred. No. 2.9e-106; Indels 0; Gaps 0;

QY 1 MALLCFCVLLGVALDRLRSLSITTPEMTEKAGETAYLPCKRPLTGPDQGDIDWILS DR 121 KVVKAPGYNKKIQLTVLKPSGRCPYDGEELGNDFLKLKCPEKEGSPLLPEWQQLSN 180

Db 1 MALLCFCVLLGVALDRLRSLSITTPEMTEKAGETAYLPCKRPLTGPDQGDIDWILS 60

QY 61 PADNOKQDVQVILLYSGDKYDDYQDLKGCRVHFTSNDLKSQDASINTNLQLSDIGTYQC DR 121 KVVKAPGYNKKIQLTVLKPSGRCPYDGEELGNDFLKLKCPEKEGSPLLPEWQQLSN 180

Db 61 PADNOKQDVQVILLYSGDKYDDYQDLKGCRVHFTSNDLKSQDASINTNLQLSDIGTYQC 120

QY 181 SOKUPTLWLAEMSPVSPVSKVNASTEYGTCTYKVNRVGSQDCLRLDVPPSNRAGTIA DR 180

Db 181 SOKUPTLWLAEMSPVSPVSKVNASTEYGTCTYKVNRVGSQDCLRLDVPPSNRAGTIA 240

QY 181 SOKUPTLWLAEMSPVSPVSKVNASTEYGTCTYKVNRVGSQDCLRLDVPPSNRAGTIA 240

OS Synthetic.
 XX KW
 PN trimerisation domain; affinity; substrate; gene therapy vector;
 XX KW infection; attachment; interaction assay; vector; monomer.
 XX OS
 PD Mastadenovirus.
 XX OS Synthetic.
 XX KW
 XX PR WO9854346-A1.
 XX PR 03-DEC-1998.
 XX PR 28-MAY-1998; 98WO-US11024.
 XX PR 16-JAN-1998; 98US-0071668.
 XX PR 28-MAY-1997; 97US-0047849.
 XX PR 03-DEC-1998.
 PA (GENV-) GENVEC INC.
 XX PR 28-MAY-1998; 98WO-US11024.
 PI Brough DE, Einfeld D, Kovesci I, Lizonova A, Roelvink PW;
 XX WICKHAM TJ, Yonehiro G;
 DR WPI; 1999-059848/05.
 DR N-PADB; AAV/2026.
 DR N-PADB; AAV/2027.
 XX PT New adenoviral fibre trimer with reduced binding to native substrate
 CC - useful for, e.g. preparing gene therapy vector with minimal
 CC ectopic infection for in vitro applications
 XX PS Example 8; Page 59-60; 103pp; English.

This sequence represents a novel adenovirus chimeric protein, SCAR.RGD. This protein is used in a method for the construction of novel monomers having an N-terminus of an adenoviral fibre protein and a trimerisation domain. Such monomers have lower affinity for native substrate than the native adenoviral fibre trimer. Cell lines containing such monomers are used (i) to propagate adenoviruses for use as gene therapy vectors (for in vitro or in vivo applications), (ii) as reagents for studying adenoviral attachment and infection, and (iii) in receptor-ligand interaction assays. The new viruses produce minimal ectopic infection (they can not infect native host cells) so are safer as vectors and can be engineered for selective targeting to other cells.

SQ Sequence 277 AA;

Query Match 84.0%; Score 1142; DB 20; Length 277;
 Best Local Similarity 88.4%; Pred. No. 2e-99; Mismatches 15; Indels 0; Gaps 0;
 Matches 214; Conservative 15; MisMatches 13; Indels 0; Gaps 0;

QY 1 MALLCFLVLLCGADLTLRSITTPQMEKAKGETAYLPCKRTLGPDQGLDIELLS 60
 1 MALLCFLVLLCGADLTLRSITTPQMEKAKGETAYLPCKRTLGPDQGLDIELLS 60
 Db QY 61 PADNQKVQVQVILLYSGDKIYDDYQDLIKGRVHFTSNDLKSGDASINTNLQLSDIGYQC 120
 61 PADNQKVQVQVILLYSGDKIYDDYQDLIKGRVHFTSNDLKSGDASINTNLQLSDIGYQC 120
 Db QY 121 KVKKAPSGVNGKKIQLTULKGPSCTRVCYDGSEEGINDPKKEPKESLPLIYEWOKLSN 180
 121 KVKKAPSGVNGKKIQLTULKGPSCTRVCYDGSEEGINDPKKEPKESLPLIYEWOKLSN 180
 Db QY 181 SOKLPTWLAEMTSPVSVKMASTEYSCYSTVKNRVSQCLRLDVPPSNRAGTIA 240
 181 SOKMPTWSLAEMLTSSVSVKNASESYGTSCTVRNRVGSQCLRLNVVPPSNKAGSGS 240
 Db QY 241 GA 242
 Db QY 241 GS 242
 RESULT 15
 AW82731 ID AW82731 standard; Protein; 397 AA.
 XX AC
 XX DT 29-MAR-1999 (first entry)
 DE Adenovirus DACSG2SCAR.sig chimERIC protein.

XX KW PACSG2SCAR.sigDEL; chimeric protein; adenoviral fibre protein;
 KW trimerisation domain; affinity; substrate; gene therapy vector;
 KW infection; attachment; interaction assay; vector; monomer.
 XX OS
 XX OS Synthetic.
 XX KW
 XX PR WO9854346-A1.
 XX PR 03-DEC-1998.
 XX PR 28-MAY-1998; 98WO-US11024.
 XX PR 16-JAN-1998; 98US-0071668.
 XX PR 28-MAY-1997; 97US-0047849.
 XX PR 03-DEC-1998.
 PA (GENV-) GENVEC INC.
 XX PR 28-MAY-1998; 98WO-US11024.
 PI Brough DE, Einfeld D, Kovesci I, Lizonova A, Roelvink PW;
 XX WICKHAM TJ, Yonehiro G;
 DR WPI; 1999-059848/05.
 DR N-PADB; AAV/2027.
 XX PT New adenoviral fibre trimer with reduced binding to native substrate
 CC - useful for, e.g. preparing gene therapy vector with minimal
 CC ectopic infection for in vitro applications
 XX PS Example 10; Page 60-62; 103pp; English.

This sequence represents a novel adenovirus chimeric protein, PACSG2SCAR.sigDEL. This protein is used in a method for the construction of novel monomers having an N-terminus of an adenoviral fibre protein and a trimerisation domain. Such monomers have lower affinity for native substrate than the native adenoviral fibre trimer. Cell lines containing such monomers are used (i) to propagate adenoviruses for use as gene therapy vectors (for in vitro or in vivo applications), (ii) as reagents for studying adenoviral attachment and infection, and (iii) in receptor-ligand interaction assays. The new viruses produce minimal ectopic infection (they can not infect native host cells) so are safer as vectors and can be engineered for selective targeting to other cells.

SQ Sequence 397 AA;

Query Match 84.0%; Score 1142; DB 20; Length 397;
 Best Local Similarity 88.4%; Pred. No. 3.4e-99; Mismatches 13; Indels 0; Gaps 0;
 Matches 214; Conservative 15; MisMatches 13; Indels 0; Gaps 0;

QY 1 MALLCFLVLLCGADLTLRSITTPQMEKAKGETAYLPCKRTLGPDQGLDIELLS 60
 1 MALLCFLVLLCGADLTLRSITTPQMEKAKGETAYLPCKRTLGPDQGLDIELLS 60
 Db QY 61 PADNQKVQVQVILLYSGDKIYDDYQDLIKGRVHFTSNDLKSGDASINTNLQLSDIGYQC 120
 61 PADNQKVQVQVILLYSGDKIYDDYQDLIKGRVHFTSNDLKSGDASINTNLQLSDIGYQC 120
 Db QY 121 KVKKAPSGVNGKKIQLTULKGPSCTRVCYDGSEEGINDPKKEPKESLPLIYEWOKLSN 180
 121 KVKKAPSGVNGKKIQLTULKGPSCTRVCYDGSEEGINDPKKEPKESLPLIYEWOKLSN 180
 Db QY 181 SOKLPTWLAEMTSPVSVKMASTEYSCYSTVKNRVSQCLRLDVPPSNRAGTIA 240
 181 SOKMPTWSLAEMLTSSVSVKNASESYGTSCTVRNRVGSQCLRLNVVPPSNKAGSGS 240
 Db QY 241 GA 242
 Db QY 241 GS 242
 RESULT 15
 AW82731 ID AW82731 standard; Protein; 397 AA.
 XX AC
 XX DT 29-MAR-1999 (first entry)
 DE Adenovirus DACSG2SCAR.sig chimERIC protein.

Wed Jul 16 14:24:18 2003

us-09-899-634c-2.rag

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:43:53 ; Search time 14 Seconds
 Sequence: (without alignments)
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Title: US-09-899-634C-2
 Perfect score: 1359
 Sequence: 1 MAILLCFVLLCGVADLIRSL.....AVIGVLALAVLGLIIFCCR 261
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database : Issued_Patents_AA:*

1: /cgn1_6/pctoda1/iaa/5A_COMB_pep: *
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 3: /cgn1_6/pctoda1/iaa/6A_COMB_pep: *
 4: /cgn1_6/pctoda1/iaa/6B_COMB_pep: *
 5: /cgn1_6/pctoda1/iaa/PCITS_COMB_pep: *
 6: /cgn1_6/pctoda1/iaa/backtles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	91.1	365	2	US-09-979-424-3
2	1238	91.1	365	4	US-09-212-496-2
3	1224	90.1	365	4	US-08-928-383B-2
4	1217	89.6	365	4	US-08-928-383B-23
5	1217	89.6	365	4	US-08-928-383B-24
6	1216	89.5	365	4	US-08-928-383B-26
7	523	38.5	106	4	US-08-928-383B-8
8	453	33.3	95	4	US-08-928-383B-17
9	351.5	25.9	273	4	US-09-214-465A-26
10	351.5	25.9	319	1	US-09-507-95B-22
11	351.5	25.9	319	4	US-09-058-051A-22
12	351.5	25.9	319	4	US-09-316-536-67
13	351.5	25.9	319	4	US-09-254-465A-6
14	341.5	25.1	270	4	US-09-234-465A-24
15	315.5	23.2	318	4	US-09-058-051A-32
16	258	19.0	319	1	US-09-175-928-2
17	246.5	18.1	394	4	US-09-336-536-39
18	244	18.0	365	4	US-09-336-536-40
19	217	16.0	319	2	US-09-979-424-1
20	199.5	14.7	249	4	US-09-336-536-42
21	196	14.4	299	4	US-09-188-930-331
22	196	14.4	299	4	US-09-402-70-2
23	196	14.4	299	4	US-09-254-465A-1
24	191	14.1	299	4	US-09-188-930-189
25	190	14.0	370	4	US-09-336-536-28
26	189	13.9	341	4	US-09-336-536-29
27	13.5				US-09-254-465A-25
28					US-09-254-465A-9
29					US-09-254-465A-23
30					US-09-152-060-76
31					US-09-254-465A-2
32					US-09-336-536-31
33					US-09-430-503-10
34					US-09-430-503-20
35					US-09-430-503-24
36					US-09-430-503-18
37					US-09-430-503-22
38					US-09-430-503-4
39					US-09-430-503-6
40					US-09-430-503-8
41					US-09-430-503-17
42					US-08-002-525-17
43					US-09-651-200-17
44					PCT-US95-025717
45					US-09-330-503-2

ALIGNMENTS

RESULT 1
 US-08-979-424-3
 Sequence 3, Application US/08979424
 Patent No. 5942606
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Corely, Neil C.
 TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto.
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/979,424
 FILING DATE: Filed Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PR-0405 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-825-0525
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLOUE: 1946351
 US-08-979-424-3

Query Match Score 1238; DB 2; Length 365;
 Best Local Similarity 89.3%; Pred. No. ie-114;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

RESULT 3
 US-08-928-383B-2
 ; Sequence 2, Application US/08928383B
 ; Patent No. 6210921
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 ; TITLE OF INVENTION: Coxsackievirus and Adenovirus
 ; NUMBER OF SEQUENCES: 26

QY 1 MALLICFVLLCGVADLTRLSTITPPEQMEKAKETAYLPCCRFTLGPDQGPDLEMILS 60
 1 MALLICFVLLCGVDFARSLSTITPPEMIEKAKGETAYLPCKFTLSPEDQGPDLEMILS 60
 Db 61 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 1 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 QY 121 KVKKAPGYNKKIQLTULKEPSGTRCYDGSSEIGNDPKLKCBPKEGSPLPLYEWQLSN 180
 1 KVKKAPGYNKKIQLTULKEPSGTRCYDGSSEIGNDPKLKCBPKEGSPLPLYEWQLSN 180
 QY 181 SOKLPTWLAEMTSPVSVRKAESTEYSGTYSCTVRNRVGSDOCLRLDVPPSNRAGTA 240
 181 SOKLPTWLAEMTSPVSVRKAESTEYSGTYSCTVRNRVGSDOCLRLDVPPSNRAGTA 240
 Db 241 GAVIGVLLALVLGLIIFCCR 261
 241 GAVIGVLLALVLGLIIFCCR 261

RESULT 2
 US-09-272-496-2
 ; Sequence 2, Application US/09272496
 ; GENERAL INFORMATION:
 ; APPLICANT: DeGregori, James
 ; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
 ; FILE REFERENCE: 90-98
 ; CURRENT APPLICATION NUMBER: US/09/272,496
 ; EARLIER FILING DATE: 1999-03-19
 ; BARLER APPLICATION NUMBER: US 60/092782
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 365
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-272-496-2

Query Match 91.1%; Score 1238; DB 4; Length 365;
 Best Local Similarity 89.3%; Pred. No. 1e-114; Indels 0; Gaps 0;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLICFVLLCGVADLTRLSTITPPEQMEKAKETAYLPCCRFTLGPDQGPDLEMILS 60
 1 MALLICFVLLCGVDFARSLSTITPPEMIEKAKGETAYLPCKFTLSPEDQGPDLEMILS 60
 Db 61 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 1 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 QY 61 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 1 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 Db 61 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 1 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 QY 121 KVKKAPGYNKKIQLTULKEPSGTRCYDGSSEIGNDPKLKCBPKEGSPLPLYEWQLSN 180
 1 KVKKAPGYNKKIQLTULKEPSGTRCYDGSSEIGNDPKLKCBPKEGSPLPLYEWQLSN 180
 Db 181 SOKLPTWLAEMTSPVSVRKAESTEYSGTYSCTVRNRVGSDOCLRLDVPPSNRAGTA 240
 181 SOKLPTWLAEMTSPVSVRKAESTEYSGTYSCTVRNRVGSDOCLRLDVPPSNRAGTA 240
 QY 241 GAVIGVLLALVLGLIIFCCR 261
 241 GAVIGVLLALVLGLIIFCCR 261

RESULT 4
 US-08-928-383B-23
 ; Sequence 23, Application US/08928383B
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 ; TITLE OF INVENTION: Coxsackievirus and Adenovirus
 ; NUMBER OF SEQUENCES: 26

QY 1 MALLICFVLLCGVADLTRLSTITPPEQMEKAKETAYLPCCRFTLGPDQGPDLEMILS 60
 1 MALLICFVLLCGVDFARSLSTITPPEMIEKAKGETAYLPCKFTLSPEDQGPDLEMILS 60
 Db 61 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 1 PADNQKVQVILYSGDKIYDDYQDLKGRRVHTTSNDIKGDASINVNLQSLDIGYQC 120
 QY 121 KVKKAPGYNKKIQLTULKEPSGTRCYDGSSEIGNDPKLKCBPKEGSPLPLYEWQLSN 180
 1 KVKKAPGYNKKIQLTULKEPSGTRCYDGSSEIGNDPKLKCBPKEGSPLPLYEWQLSN 180
 Db 181 SOKLPTWLAEMTSPVSVRKAESTEYSGTYSCTVRNRVGSDOCLRLDVPPSNRAGTA 240
 181 SOKLPTWLAEMTSPVSVRKAESTEYSGTYSCTVRNRVGSDOCLRLDVPPSNRAGTA 240
 QY 241 GAVIGVLLALVLGLIIFCCR 261
 241 GAVIGVLLALVLGLIIFCCR 261

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/928,383B
 FILING DATE: 12-SEP-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,100
 FILING DATE: 13-SEP-1996

ATTORNEY / AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids

SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-928-383B-23

Query Match 89.6%; Score 1217; DB 4; Length 365;
 Best Local Similarity 88.1%; Pred. No. 1.2e-112; Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MAUUCFVLLCGVADLRSLSITPPEOMIEKAKGETAYLPICRTLGPDQPLDIEWLS 60
 Db 1 MARLUCCFVLLCGIADFTSGSLITTPPEORIEKAKGETAYLPCKFTLSPEDOGPLDIEWLS 60

Qy 61 PADNQKDQVILYSPKIVYDQDLKGGRVHTFTSNDLKGASINTVNQLSDIGTYQC 120
 Db 61 PSDNQIVDQVILYSGDKIVNYYPDLKGGRVHTFTSNDVKGSDASINTVNQLSDIGTYQC 120

Qy 61 PADNQKDQVILYSPKIVYDQDLKGGRVHTFTSNDLKGASINTVNQLSDIGTYQC 120
 Db 61 PSDNQIVDQVILYSGDKIVNYYPDLKGGRVHTFTSNDVKGSDASINTVNQLSDIGTYQC 120

Qy 61 PSDNQIVDQVILYSGDKIVNYYPDLKGGRVHTFTSNDVKGSDASINTVNQLSDIGTYQC 120
 Db 61 PSDNQIVDQVILYSGDKIVNYYPDLKGGRVHTFTSNDVKGSDASINTVNQLSDIGTYQC 120

Qy 121 KVKKAPGIVGNKKIQLTVLKPSTRCVGDSEBIGNDFKLKEPKEGSSLPLIYEWORKLSN 180
 Db 121 KVKKAPGIVGNKKIQLTVLKPSTRCVGDSEBIGNDFKLKEPKEGSSLPLIYEWORKLSN 180

Qy 181 SQKLTPLWLAEMTSPVSVKNASTEYSGTSCVTVKRVSQCLRLDVVPNSRAGTIA 240
 Db 181 SQKLTPLWLAEMTSPVSVKNASTEYSGTSCVTVKRVSQCLRLDVVPNSRAGTIA 240

Qy 181 SQKLTPLWLAEMTSPVSVKNASTEYSGTSCVTVKRVSQCLRLDVVPNSRAGTIA 240
 Db 181 SQKLTPLWLAEMTSPVSVKNASTEYSGTSCVTVKRVSQCLRLDVVPNSRAGTIA 240

Qy 241 GAVIGVLLALVGLIIFCC 260
 Db 241 GAVIGVLLALVGLIIFCC 260

RESULT 5
 US-08-928-383B-24
 Sequence 24, Application US/08928383B
 Patent No. 6210921

GENERAL INFORMATION:
 APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 TITLE OF INVENTION: CAR, A NO. 6210921el Coxsackievirus and Adenovirus

APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA

RESULT 6
 US-08-928-383B-26
 Sequence 26, Application US/08928383B
 Patent No. 6210921

GENERAL INFORMATION:
 APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 TITLE OF INVENTION: CAR, A NO. 6210921el Coxsackievirus and Adenovirus

APPLICANT: and Marshall S. Horwitz
 TITLE OF INVENTION: CAR, A NO. 6210921el Coxsackievirus and Adenovirus

APPLICANT: and Marshall S. Horwitz
 TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA

ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,383B
 FILING DATE: 12-SEP-1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,100

FILING DATE: 13-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-928-383B-26

Query Match 89.5%; Score 1216; DB 4; Length 365;
 Best Local Similarity 88.1%; Pred. No. 1. 1.e-11;
 Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAJLLCFULLGYADLRTSLSITPEQMEKAKGETAYLPCKRTLGPDQGPIDEWILS 60
 Db 1 MARLICFLIGGIADFTSGSISITPEOKEIKAKGETAYLPCKRTLSPDQGPIDENLIS 60

QY 61 PAQNQKVQVILLYSGDKIYDDYQDLKGVRHFTSDNJKSGDASINVNLQLSDIGTYQC 120
 Db 61 PSDNQIVDQVILLYSGDKIYDDYQDLKGVRHFTSDNJKSGDASINVNLQLSDIGTYQC 120

QY 121 KVKKAPCGVNNKKIQLTUVLKPSCTRCVYDGESETIGNDKLKCPCPKESLPLPYEWOKLSN 180
 Db 121 KVKKAPGVANKKQLLTUVLKPSCTRCVYDGESETIGNDKLKCPCPKESLPLPYEWOKLSN 180

QY 181 SQKUPTLMAEMTSPVNSVKAESTEYSGTYSCTVKNRVGSQCLLRDVPPSNRAGIA 240
 Db 181 SQKUPTLMAEMTSPVNSVKAESTEYSGTYSCTVKNRVGSQCLLRDVPPSNRAGIA 240

QY 241 GAVIGVLUAVLVLGLIIFCC 260
 Db 241 GAVIGVLUAVLVLGLIIFCC 260

RESULT 7
 US-08-928-383B-8

Sequence 8 Application US/08928383B
 Patent No. 6210921

GENERAL INFORMATION:
 APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 APPLICANT: and Marshall S. Horwitz
 TITLE OF INVENTION: Receptor, A No. 6210921el Coxsackievirus and Adenovirus
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA

ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,383B
 FILING DATE: 12-SEP-1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,100

FILING DATE: 13-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

APPLICATION NUMBER: US 60/026,100
 FILING DATE: 13-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,100

ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

APPLICATION NUMBER: US 60/026,100
 FILING DATE: 13-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 95 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-09-928-383B-17

Query Match 33.3%; Score 453; DB 4; Length 95;
 Best Local Similarity 87.4%; Pred. No. 1.1e-37; Matches 83; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 141 PSCTRCVGDSEBIGNDKLKCEPKEGSILPLIYEWOKLNSOKPLTMLAEMTSPVSVK 200
 Db 1 PSGARCYVDGSEBISGSPFKICKEPKEGSILPLQYEWOKLSDQKMTSPVSLWEMTSSVSVK 60

Qy 201 NASTEVSYSTCIVKRNVRGSDQCLLRDGVPPSNR 235
 Db 61 NASSESYSTCIVKRNVRGSDQCLLRDGVPPSNK 95

RESULT 9
 US-09-254-465A-26
 Sequence 26, Application US/09254465A
 Patent No. 6410708
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Fong, Sherman
 APPLICANT: Goddard, Andrew
 APPLICANT: Gurney, Austin L.
 APPLICANT: Napier, Mary A.
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
 FILE REFERENCE: P1216RA(US)
 CURRENT APPLICATION NUMBER: US/09/254, 465A
 CURRENT FILING DATE: 1999-03-05
 PRIOR APPLICATION NUMBER: PCT/US98/24855
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: US 60/066, 364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: US 60/078, 936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: PCT/US98/19437
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO 26
 LENGTH: 273
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-254-465A-26

Query Match 25.9%; Score 351.5; DB 4; Length 273;
 Best Local Similarity 34.1%; Pred. No. 5.8e-27; Matches 89; Conservative 53; Mismatches 96; Indels 23; Gaps 11;

Qy 10 LCGVADLRTSLSTTPOMIEKAKGETAYLPCKTFGLPBDQSPDLSM--LLSPADNQK 66
 Db 1 LCACVRTVDAISVETPQDVLRASQGSVTLPCRTHTSTSREGI-IQWDKLNT---H 54

Qy 67 VDQVILLYSGDK-IYDDYQDQLGKRQHFTPSNDLKGQDASINVNLQLSDIGTYQCKVK 124
 Db 66 TERVVITWPFNSKNYIHGELY--KNRVS1-SNNAEQSDASITIDOLTMADNGTYECVSVL 121

Qy 125 ARGV-GNKK-IQLTWILKPSTRCYVDGSEBIGNDKLKCEPKEGSILPLIYEWOKLNS-N 180
 Db 122 MSDLEGNTKSRVRLVLUVPPSKPECIGEGETIGNNIQLTCOSKEGSPTPQSWKVNIL 181

Qy 181 SQKPLTMLAEMTS-PVISKVNAESTSGTSCTVNRVGSDOCLLRDGVPPSNRAGTI 239
 Db 182 NOEQP--LAQPASGPQDVSLKNIOTSGYVICTSSNEGTOFCNITVAVRSPSMWALY 238

181 SQKPLTMLAEMTS-PVISKVNAESTSGTSCTVNRVGSDOCLLRDGVPPSNRAGTI 239

RESULT 10
 US-08-597-495B-22
 Sequence 22, Application US/08597495B
 Patent No. 5712369
 GENERAL INFORMATION:
 APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
 APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
 APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
 APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
 TITLE OF INVENTION: Colon Cell And Colon Cancer Cell Associated Nucleic Acid Molecules, Protein And Peptides
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Relife & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/597, 495B
 FILING DATE: 02-Feb-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, NO. 5712369man D.
 REGISTRATION NUMBER: 30, 946
 REFERENCE/DOCKET NUMBER: LUD 5316.1
 PRIORITY DATA:
 APPLICATION NUMBER: 08/511, 876
 FILING DATE: 04-Aug-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, NO. 5712369man D.
 REGISTRATION NUMBER: 30, 946
 REFERENCE/DOCKET NUMBER: LUD 5316.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-2200
 TELEFAX: (212) 838-3894
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 319 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 TOPOLOGY: linear
 US-08-597-495B-22

Query Match 25.9%; Score 351.5; DB 1; Length 319;
 Best Local Similarity 34.1%; Pred. No. 7.3e-27; Matches 89; Conservative 53; Mismatches 96; Indels 23; Gaps 11;

Qy 10 LCGVADLRTSLSTTPOMIEKAKGETAYLPCKTFGLPBDQSPDLSM--LLSPADNQK 66
 Db 12 LCAVVRTVDAISVETPQDVLRASQGSVTLPCRTHTSTSREGI-IQWDKLNT---H 54

Qy 67 VDQVILLYSGDK-IYDDYQDQLGKRQHFTPSNDLKGQDASINVNLQLSDIGTYQCKVK 124
 Db 66 TERVVITWPFNSKNYIHGELY--KNRVS1-SNNAEQSDASITIDOLTMADNGTYECVSVL 121

Qy 125 ARGV-GNKK-IQLTWILKPSTRCYVDGSEBIGNDKLKCEPKEGSILPLIYEWOKLNS-N 180
 Db 122 MSDLEGNTKSRVRLVLUVPPSKPECIGEGETIGNNIQLTCOSKEGSPTPQSWKVNIL 181

Qy 181 SQKPLTMLAEMTS-PVISKVNAESTSGTSCTVNRVGSDOCLLRDGVPPSNRAGTI 239
 Db 182 NOEQP--LAQPASGPQDVSLKNIOTSGYVICTSSNEGTOFCNITVAVRSPSMWALY 238

QY 240 AGAVIVGVLALVVLIGLIFCC 260
Db 239 VGLAVGVVAAALIIGIIVCC 259

RESULT 11
US-09-068-051A-22
; Sequence 22, Application US/09068051A
; Patent No. 6,291,235
; GENERAL INFORMATION:
; APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
; Catimel, B.; Ji, Hong; Burgess, Anthony W.;
; Heath, Joan K.; White, Sara J.; Johnstone, Cameron
; TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,051A
; FILING DATE: 10 Dec-1998
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/597,495
; REFERENCE DOCKET NUMBER: IUD 5316.2
; FILING DATE: 02-Feb-1996
; APPLICATION NUMBER: 08/511,876
; FILING DATE: 04-Aug-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6291235man D.
; REGISTRATION NUMBER: 30,946
; TELEPHONE: (212) 318-3188
; TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22
; US-09-068-051A-22

Query Match 25.9%; Score 351.5; DB 4; Length 319;
Best Local Similarity 34.1%; Pred. No. 7.3e-27; Indels 23; Gaps 11;
Matches 89; Conservative 53; Mismatches 96; Deletes 23; Gaps 11;

QY 10 LCGVADLRLSLSITPQOMIEKAKGETAYLPQRFTLGPEDQPLDIEW--LLSPADNQ 66
Db 12 LCAGVAVTDAISETPDQDLRASQSKVLPYHTTSRSGI-1QWDKLIL---H 65

QY 67 VDQVILYLGS GDK--IYDYYQDQIKGRVHTPSNLKSDASINTNQLQSDIGTYQCKVK 124
Db 66 TERVINWPSNKNVIBESLY--KRNSI-SNAEBSASITDOLTMADNTYECVSL 121

QY 125 APGV-GNKK-TOLTIVLKPGSTRCYVGSEEIGNDFLKICPEKGSSLPLYEWOKS-N 180
Db 122 MSDELEGNTKSRVRLLVLPSPKPEGIETTIGNNQLTCOSKEGSPPTPOYSWKRYNL 181

QY 181 SOKLPLTMLAEMTS-PVLSVKASTEVSGTWSCTVKVRVGSQCLLDVVPSPNRAGTI 239
Db 182 NQROP---LAQPASQPVSLKVNSTDPSGYVICTSSNEEGTOFCNITVAVRSPSMNVALY 238

QY 240 AGAVIVGVLALVVLIGLIFCC 260
Db 239 VGLAVGVVAAALIIGIIVCC 259

RESULT 13
US-09-254-465A-6
; Sequence 6, Application US/09254465A
; Patent No. 6,410,708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Andrew
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P-216R(US)

CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,336

PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 6
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-6

Query Match 25.9%; Score 351.5; DB 4; Length 319;
Best Local Similarity 34.1%; Pred. No. 7.3e-27;
Matches 89; Conservative 53; Mismatches 96; Indels 23; Gaps 11;

Qy 10 ICGVADLRLSITTEPQMIEKAKGETAYLPCRFGLPBDQPLDIEW--LLSPDNQK 66
Db 12 ICAVRVTDALSIETPQDVLRAQSOKSYTLPCTYHTSREGI-TQWDKLLT---H 65

Qy 67 VDQVITLNSGDK--IYDYYQDLKGRAFTSDNLKGDASINTNQLSDIGTYQCKVK 124
Db 66 TERWVIMPPFSKNKYIHGELY--KRNSI-SNNAEQSDASITIDOLTMADNGTYECVSVL 121

Qy 125 AFGV-GNKK--IQLTVLKPSCTRVCYDGESEIGNDFKLKCPKEGSPLPYEWOKLS-N 180
Db 122 MSDLEGNTKSRYVLLVLVPPSKPECIGEGETIGNNIQLTCQSKBSPPTQOYSWKRNIL 181

Qy 181 SOKLPTWLAMEITS-PVIVSKVASTENSGYISCTVKRUGVSDQCLRLDVVPPSNRAGTI 239
Db 182 NQEQP--LAQFASQGQRVSLKVNISTDTGIVYCTSSNEGTQFCNITVAVRSPSMNVALY 238

Qy 240 AGAVIGVLLAVLVLIGLIFC 260
Db 239 VGIAGVGVVAALIIGIYCC 259

RESULT 14
US-09-254-465A-24
Sequence 24, Application US/09254465A
Patent No. 6410708

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT OF DISEASES CHARACTERIZED BY AB33- RELATED ANTIGENS

FILE REFERENCE: P1216R1(US)

CURRENT APPLICATION NUMBER: US/09/254,465A

CURRENT FILING DATE: 1999-03-05

PRIOR APPLICATION NUMBER: PCT/US98/24855

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: US 60/066,364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 60/078,936

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: PCT/US98/19437

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 24
LENGTH: 270
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-24

RESULT 15
US-09-068-051A-32
Sequence 32, Application US/09068051A
Patent No. 6281235

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Catinel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron

TITLE OF INVENTION: Colon Cell And Colon Cancer Cell Associated Nucleic Acid Molecules, Protein And Peptides

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996

APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6291235man D.
REGISTRATION NUMBER: 30,946
REFERENCE DOCKET NUMBER: LUD 5316.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-9958

INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-068-051A-32

Query Match 25.1%; Score 341.5; DB 4; Length 270;
Best Local Similarity 34.1%; Pred. No. 5.6e-26;
Matches 86; Conservative 53; Mismatches 90; Indels 23; Gaps 11;

Qy 19 SLSITTPBOMIKRAGETAYLPCRFGLPBDQPLDIEW--LLSPDNQKVQVILYS 75

Qy 7 AISVETQDVIRASQGKSVTPTVITTSREGL IOWDKLLT---HTERVVWPF 60
Db 76 GDK-TYDDYQDPLKGERVHFTSNDLKSASINVTMQLSIGHTYQCKVKKAPGV-GNKK 132
Qy 61 SNKNYIIGELY--KQFVSI-SNNAEQSDASITIDOTMAUNGTYECSVLSMSDIEKT 116
Db 133 --IQLTWLKPQGTRCVGDGSEEIGNDFKLKCPKEGSPLPYEWOKLS-NSQKPLTLW 189
Db 117 SRVRLVLLVPRSKPECIGEGETIGNNIQLTCQSKBSPPTQOYSWKRYTNLOEQP---L 173
Db 190 AEMTS-PVISVKVNSTASYGTYISCTVNNRVSQDCLRLDVVPPSNRAGTIAVGIVVLL 248
Db 174 AOPASCPVSLXNISTDTGIVYCTSSNEGTQFCNITVAVRSPSMNVALYVGIAVGVVA 233
Db 249 ALVLLIGHTIFCC 260
Db 234 AIIIGIYIYCC 245

Qy 9 LLGQVADLRLSITTEPQMIEKAKGETAYLPCRFGLPBDQPLDIEW--LLSPDNQKVQVILYS 66

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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:44:38 : Search time 23 Seconds
(without alignments)
1321.111 Million cell updates/sec

Title: US-09-899-634C-2
Perfect score: 1359
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Scoring table: BLOSUM62
Gappp 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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10: /cgn2_6/podata/1/pupbaa/US09_PUBCOMB.pep:*

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12: /cgn2_6/podata/1/pupbaa/US10_PUBCOMB.pep:*

13: /cgn2_6/podata/1/pupbaa/US60_NEW_PUB.pep:*

14: /cgn2_6/podata/1/pupbaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	1359	100.0	261	10	US-09-899-634A-2	Sequence 2, Applied
2	1353	99.6	365	10	US-09-899-634A-4	Sequence 4, Applied
3	1238	91.1	352	9	US-09-992-598-505	Sequence 505, App
4	1238	91.1	352	9	US-09-988-293A-505	Sequence 505, App
5	1238	91.1	352	9	US-09-989-733-505	Sequence 505, App
6	1238	91.1	352	9	US-09-990-441-505	Sequence 505, App
7	1238	91.1	352	9	US-10-053-101-10	Sequence 10, Applied
8	1238	91.1	352	9	US-09-939-730-505	Sequence 505, App
9	1238	91.1	352	9	US-09-930-436-505	Sequence 505, App
10	1238	91.1	352	9	US-09-931-183-505	Sequence 505, App
11	1238	91.1	352	9	US-09-933-687-505	Sequence 505, App
12	1238	91.1	352	9	US-09-939-734-505	Sequence 505, App
13	1238	91.1	352	9	US-09-997-653-505	Sequence 505, App
14	1238	91.1	352	9	US-09-933-667-505	Sequence 505, App
15	1238	91.1	352	9	US-09-930-380-505	Sequence 505, App
16	1238	91.1	352	9	US-09-990-562-505	Sequence 505, App
17	1238	91.1	352	9	US-09-997-420-505	Sequence 505, App
18	1238	91.1	352	9	US-09-997-666-505	Sequence 505, App
19	1238	91.1	352	9	US-10-227-884-216	Sequence 216, App

ALIGNMENTS

RESULT 1
US-09-899-634A-2
; Sequence 2, Application US/09899634A
; Patent No. US2002009634A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gaident, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: PCR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09-899,634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: porcine
; US-09-899-634A-2

Query Match 100.0% ; Score 1359; DB 10; Length 261;
Best local similarity 100.0%; Pred. No. 4 Se-89;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLICFVILCGVADLTRLSLITPEOMIEKAGETAYLPCREFTLGPEQGPIDEWLS 60
Db 1 ||||||| MALLICFVILCGVADLTRLSLITPEOMIEKAGETAYLPCREFTLGPEQGPIDEWLS 60
QY 61 PADNQKVDPVILYSGDKTYDQDLKGRVRHTSNDIJKSGDASINVNLQLSDIGTQC 120
Db 61 PADNQKVDPVILYSGDKTYDQDLKGRVRHTSNDIJKSGDASINVNLQLSDIGTQC 120
QY 121 KVKKAPAGVNKKQIQLTVLKPSCTRYCDGSEIGNDPLKCKPKEGSPLPLWQKSN 180
Db 121 KVKKAPAGVNKKQIQLTVLKPSCTRYCDGSEIGNDPLKCKPKEGSPLPLWQKSN 180
QY 181 SOKLPTLMLAEMSPVTISKNASTEYSGTSCTVKNRVGSQDLRLRUVPPSNRAGTIA 240
Db 181 SOKLPTLMLAEMSPVTISKNASTEYSGTSCTVKNRVGSQDLRLRUVPPSNRAGTIA 240
QY 241 GAVIVGLALVLIGLIFCCR 261
Db 241 GAVIVGLALVLIGLIFCCR 261

RESULT 2
US-09-899-634A-4
; Sequence 4, Application US/0999634A
; Patent No. US20056654A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Bluhler, Reto Andreas Gradient, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: PCR and its uses
; FILE REFERENCE: 4-3499A
; CURRENT APPLICATION NUMBER: US/09/899, 634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 4
; LENGTH: 365
; TYPE: PRT
; ORGANISM: porcine
; US-09-899-634A-4

Query Match 99.6%; Score 1353; DB 10; Length 365;
Best Local Similarity 99.6%; Pred. No. 1.7e-88;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLICFVILCGVADLTSLSITPEQMIEKAKGETAYLFCRFLGPDQGPDIDWLS 60
Db 1 MALLICFVILCGVADLTSLSITPEQMIEKAKGETAYLFCRFLGPDQGPDIDWLS 60
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087595
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11

RESULT 3
US-09-992-598-505
; Sequence 505, Application US/09992598
; Patent No. US2002163384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber-Hansperger
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
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; PRIOR APPLICATION NUMBER: 60/089532
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/090694

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; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80; Mismatches 15; Indels 0; Gaps 0;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy	1	MALLCPCVLLCGVADITRSISITTEBQMIEKAGETAYLPCTRFITGPEDOCPLDTEWLLS	60
Db	1	MALLCPCVLLCGVVDPARSLSITTBEMIEKAGETAYLPCKFTLSPEDQGPLDIEWLLS	60
Qy	61	PADNQKVQWVILYLSKDKIYDYQDQKGRTHTFSNDLKGSDASINTNLQSLDGTYQC	120
Db	61	PADNQKVQDVQVILYLSKDKIYDYQDQKGRTHTFSNDLKGSDASINTNLQSLDGTYQC	120
Qy	121	KUKKAPCGVGNKKIQLTULLKEPSGTRCYVDGSEBEIGNDFKLKCEPKBEGSLPLUYEWKLNS	180
Db	121	KUKKAPCGVANKEKTHLULVKRSGARCYDVDESEEIGSDFKIKCEPKBEGSLPLUYEWKLNS	180
Qy	181	SOKLPTMILWALMNTSPVSVKRASTEYGTSTCVKNRRVGSDOCLRLDWWPPSNRAGTIA	240
Db	181	SOKMPTSWLAENTSSYISKNSASSEYSITSCVTVRNRVGSDOCLRLNWWPPSNKAGLIA	240
Qy	241	GAVIGVIALVALVIGLITFCCR	261
Db	241	GAIGITLALALIGLIFCCR	261

RESULT 4
US-09-989-293A-505
; Sequence 505, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: KJavvin, Ivar J.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730P1C6

CURRENT APPLICATION NUMBER: US/09/989, 293A

PRIOR FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/0499787

PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1998-07-09 ;

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MAILCFULLGYADLRTSLSLITPQEONIKRKGAKGETAYLPCKRFTEGFDQGDLEWLLS 60 ;
Db 1 MAUJLCFULLGYDFAKSLSLITPQEONIKRKGAKGETAYLPCKRFTEGFDQGDLEWLLS 60 ;
Qy 61 PADNOKVQVIIYSGDKIYDDYQDLGRVRHTSDNLKGSASINTNLQSDIGYQC 120 ;
Db 61 PADNOKVQVIIYSGDKIYDDYQDLGRVRHTSDNLKGSASINTNLQSDIGYQC 120 ;
Qy 121 KVKKAPGVNKKIQLTVLKLPGSGTRCYVDGSEBINGDFKLKCEPKESLPLIYEWOKLN 180 ;
Db 121 KVKKAPGVNKKIHLWVLVPSARCYVGDSSEBGSFPKICPKBESLPLQYEWOKLSD 180 ;
Qy 181 SQQLPTLMLAEMTSPVLSVRASTEYSGTSCTVKNRVGSDOCLRLDVPPSNRACTIA 240 ;
Db 181 SQQLPTLMLAEMTSPVLSVRASTEYSGTSCTVKNRVGSDOCLRLDVPPSNACTIA 240 ;
Qy 241 GAVIGVLLALVLGLIICCR 261 ;
Db 241 GATIGTGLLALALGLIFCCR 261 ;

RESULT 5
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; Sequence 505, Application US/09989735
; Publication No. US2002013299A1
; GENERAL INFORMATION:
; APPLICANT: Asikenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIPC61
; CURRENT APPLICATION NUMBER: US/09/989, 735
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 PRIOR APPLICATION NUMBER: 60/091978 ;
 PRIOR FILING DATE: 1998-07-07 ;
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 PRIOR FILING DATE: 1998-07-09 ;

;

Query Match 91.1%; Score 1238; DB 9; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.3e-80;
 Matches 233; Consistency 13; Mismatches 15; Insets 0; Gaps 0;

Qy	1	MALLCIVLCCVADITRSLSITPQQMEKAGETAYLPGRFTLGPDQPLDEWLLS	60
Dy	1	MALLCIVLCCVDFARSLSTTPEEMIEKAGETAYLPCKFTLSFPEDQPLDIEWLLS	60
Qy	61	PADNQKDQVILYSDKIKYDQYQDQKGRHTFSMDLKGSDASINTNQLSDIGTYQC	120
Dy	61	PADNQKDQVILYSGDVKYDQPKGRVHTFSMDLKGSDASINTNQLSDIGTYQC	120
Qy	121	KYKKAPSYGNKKIQLTULLKGSGTRCYDGSBEIGNDFKLKCEPKGSSLPLIYWMKLN	180
Dy	121	KYKKAPSYGNKKIQLTULLKGSGTRCYDGSBEIGNDFKLKCEPKGSSLPLIYWMKLN	180
Qy	181	SOKLPTWLAEMTSPTSVKRASTEVGTSCTVKVRGSPNCLRLDVVPSPNSNRAGTIA	240
Dy	181	SOKLPTWLAEMTSVSVKRASESVGTSCTVRNVSQDCLRLNVVPSNKGALLIA	240
Qy	241	GAVIGVIALVIGLIFCCR	261
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RESULT 6
 US-09-990-444-505

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		PRIOR APPLICATION NUMBER: 60/088326
	GENERAL INFORMATION:	PRIOR FILING DATE: 1998-06-04
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	APPLICANT: Desnoyers, Luc	PRIOR FILING DATE: 1998-06-05
	APPLICANT: Eaton, Dan L.	PRIOR APPLICATION NUMBER: 60/088212
	APPLICANT: Ferrara, Napoleone	PRIOR FILING DATE: 1998-06-10
	APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/088217
	APPLICANT: Gerber, Hanspeter	PRIOR FILING DATE: 1998-06-10
	APPLICANT: Gerritsen, Mary E.	PRIOR APPLICATION NUMBER: 60/088655
	APPLICANT: Goddard, Audrey	PRIOR FILING DATE: 1998-06-09
	APPLICANT: Grimaldi, J Christopher	PRIOR APPLICATION NUMBER: 60/088734
	APPLICANT: Gurney, Austin L.	PRIOR FILING DATE: 1998-06-10
	APPLICANT: Kljavin, Ivar J.	PRIOR APPLICATION NUMBER: 60/088738
	APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
	APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088742
	APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
	APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088810
	APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-10
	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/088861
	FILE REFERENCE: P2730PC19	PRIOR FILING DATE: 1998-06-11
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 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
 Best Local Similarity 87.3%; Pred. No. 2,3e-80;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLICFVILCGVADLTRLSITPEQMTEKAKGETAYLPCRFITLGPDQGPDIEMWLLS
 Db 1 MALLICFVILCGVADLTRLSITPEQMTEKAKGETAYLPCRFITLGPDQGPDIEMWLLS 60
 QY 61 PADNOKVQDVTIYLSGDKYDDYQDLKGKRVHFSNDLJGGSASINVNLQLSDIGTVQC
 Db 61 PADNOKVQDVTIYLSGDKYDDYQDLKGKRVHFSNDLJGGSASINVNLQLSDIGTVQC 120
 QY 181 SQKUPTLWIAEMLTSPVSIKNASTEYSGTYSCTVKNRVQSDQCLRLDVPPSNRAGTA 240
 Db 121 KVKGKAPGVNKKIQLTVLKPGRCTRYGDSSEETGNDFKLKCERKEGSIPLPYEWOKLSN 180
 Db 121 KVKGKAPGVNKKIHLVLYVKPSGARCYVGSEEGSDFKKICKEPKEGSLPQZEWOKLSD 180
 QY 181 SQKUPTLWIAEMLTSPVSIKNASTEYSGTYSCTVKNRVQSDQCLRLDVPPSNRAGTA 240

RESULT 7
 US-10-053-107-10
 Sequence 10, Application US/10053107
 ; Publication No. US20020192752A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goddard,Audrey
 ; APPLICANT: Godowski,Paul J.
 ; APPLICANT: Gurney,Austin L.
 ; APPLICANT: Hillan,Kenneth J.
 ; APPLICANT: Tumas,Daniel
 ; APPLICANT: Watanabe,Colin K.
 ; APPLICANT: Wood,William I.
 ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 ; Title of Invention: Related Diseases
 ; FILE REFERENCE: P203R1C1
 ; CURRENT APPLICATION NUMBER: US/10/053,107
 ; CURRENT FILING DATE: 2002-01-17
 ; PRIOR APPLICATION NUMBER: 60/099601
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/107783
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: 60/108802
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 ; PRIOR APPLICATION NUMBER: 60/113296
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 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 09/218517
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 ; PRIOR FILING DATE: 1999-01-05
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 ; PRIOR FILING DATE: 1999-09-01
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 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/05601
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/13705
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 ; PRIOR APPLICATION NUMBER: PCT/US00/14941
 ; PRIOR FILING DATE: 2000-05-30
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21066
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 14

SEQ ID NO: 10
 LENGTH: 352
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-053-107-10

Query Match	Best Local Similarity	Score	DB	Length
Matches 233; Conservative	91.1%; 13; Mismatches	1238; 9;	9;	352;
		Pred. No. 2; 3e-80;		
		Indels 0; gaps 0;		
Qy	1 MALLCFVULCGVADLRSLSITTPBQMEKAKGETAYLPICRFTGPGDQGLDIEULLS	60		
Db	1 MALLCFVULCGVUDFARSLSITTPBEMEIKAKGETAYLPICRFTGPGDQGLDIEULLS	60		
Qy	61 PADNQKVQDVILLYSGDKIYDDYQDLKGRVRHTSDNLSNDKGDASINTNLQLSDIGTYQC	120		
Db	61 PADNQKVQDVILLYSGDKIYDDYQDLKGRVRHTSDNLSNDKGDASINTNLQLSDIGTYQC	120		
Qy	121 KVVKAPSGVNGKKIQLTVLKLPGSTRCYVDGSEBIGNPFLKLKEPKBSLPLIYEWQKLSN	180		
Db	121 KVVKAPGVANKKHLVVLVKPSGRCYVGDSEBGSDFKIKCBEPKESLPLIYEWQKLSN	180		
Qy	181 SOKLPTLMLAEMTSPVSVNASTEYSGTSCVNRVGSQCLLRDVVPPSNRAGTIA	240		
Db	181 SQKNTPSLMLAEMTSPVSVNASTEYSGTSCVNRVGSQCLLRDVVPPSNRAGTIA	240		
Qy	241 GAVTGVLALVLGILIFCCR	261		
Db	241 GAIGTTLALALALIGLIFCCR	261		

RESULT 8

US-09-989-730-505

Sequence 505, Application US/09989730

Publication No. US20020197674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritzen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Guiney, Austin L.

APPLICANT: Klijavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730PIC69

CURRENT APPLICATION NUMBER: US/09/989,730

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/088861

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/088876

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/089105

PRIOR FILING DATE: 1998-06-12

PRIOR APPLICATION NUMBER: 60/089340

PRIOR FILING DATE: 1998-06-16

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PRIOR FILING DATE: 1998-06-16

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PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/079110

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

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 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02

; PRIOR FILING DATE: 1998-07-09
 Query Match 91.1%; Score 1238; DB 9; length 352;
 Best Local Similarity 89.3%; Pred. No. 2.3e-80;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db		
1 MALLCFCVLLGGVADLTSRSLITTPEMIEKAGEFAYLPRLPFTLGEDQGDIDLEULLS 60	1 MALLCFCVLLGGVNDPARSLITTPEMIEKAGEFAYLPRLPFTLSPEDQGPDIBELIS 60	61 PADNQKYDQVILYLYSDKIVYYDQYOLKGRRHTTSNDKSDASINTVNLUOLSDIGYQC 122	61 PADNQKVDTQVILYLYSDKIVYYDQYOLKGRRHTTSNDKSDASINTVNLUOLSDIGYQC 122	121 KUKKAPBQGNKKIQLTVLKSGTRCYDGSBEGIDFKLKECPKGSPLPYEWQLSN 188	121 KUKKAPBQGNKKIQLTVLKSGTRCYDGSBEGIDFKLKECPKGSPLPYEWQLSN 188	121 KYKARGVANKKHLVVLVKPSGRCVTDGSBEEIGSDFKIKCPKGSPLPYEWQKLSD 188	121 KYKARGVANKKHLVVLVKPSGRCVTDGSBEEIGSDFKIKCPKGSPLPYEWQKLSD 188	181 SQKLPTWLAETMTPSVKRASTESGTYCTVKURVGSDQCLLRIDVVPSNRAGTIA 249	181 SQKLPTWLAETMTPSVKRASTESGTYCTVKURVGSDQCLLRIDVVPSNRAGTIA 249	181 SQKMPPTSWLAETMSSVSYVKRASESGTYSCTVRNRVGSDQCLLRILANVPSPNAGLIA 249	181 SQKMPPTSWLAETMSSVSYVKRASESGTYSCTVRNRVGSDQCLLRILANVPSPNAGLIA 249
Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db		
181 SQKLPTWLAETMTPSVKRASTESGTYCTVKURVGSDQCLLRIDVVPSNRAGTIA 249	181 SQKLPTWLAETMTPSVKRASTESGTYCTVKURVGSDQCLLRIDVVPSNRAGTIA 249	181 SQKMPPTSWLAETMSSVSYVKRASESGTYSCTVRNRVGSDQCLLRILANVPSPNAGLIA 249	181 SQKMPPTSWLAETMSSVSYVKRASESGTYSCTVRNRVGSDQCLLRILANVPSPNAGLIA 249	241 GAVIVGVLLALVGLIIFCCR 261	241 GAVIVGVLLALVGLIIFCCR 261	241 GATIGTLLALALAGLIIIFCCR 261	241 GATIGTLLALALAGLIIIFCCR 261				

RESULT 9
 US-09-990-436-505
 ; Sequence 505, Application US/09990436
 ; Publication No. US200202198148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Askenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Klijavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watnabb, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William T.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C14
 ; CURRENT APPLICATION NUMBER: US/09-990-436

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80; Mismatches 15; Indels 0; Gaps 0;

Matches 233; Conservative 13; MisMatches 15; Indels 0; Gaps 0;

Y 1 MALLUCFVLUUGVADLRTSLSITTEPQMEBKAKGCTAYLPCREFTLGPEOGPADIEWLIS 60
b 1 MALLUCFVLUUGVADLRTSLSITTEPQMEBKAKGCTAYLPCREFTLGPEOGPADIEWLIS 60
Y 61 PADNQKUDPOVILYSGDKYIYDYYQDLKGVRHFTSNDLSSGASINVNLQLSPDTQC 120
b 61 PADNQKUDPOVILYSGDKYIYDYYQDLKGVRHFTSNDLSSGASINVNLQLSPDTQC 120
Y 121 KUKKAPGPGVKKIQITVLLPKSGRGRCYDSEEIGANDFLKLCKCEKEGSPLPLNEWOKSN 180
b 121 KUKKAPGPGVKKIQITVLLPKSGRGRCYDSEEIGANDFLKLCKCEKEGSPLPLNEWOKSN 180
Y 181 SOKLPTWLAEMTSRVSIVKASTBYGSTYCTVKNRVSDOCLRLDVPPSNRAGTIA 240
b 181 SOKLPTWLAEMTSRVSIVKASTBYGSTYCTVKNRVSDOCLRLDVPPSNRAGTIA 240
Y 241 GAVIGVLLAVLIGLIIFCCR 261
b 241 GAVIGVLLAVLIGLIIFCCR 261
RESULT 10
S 09-991-181-505
Sequence 1505, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Boststein, David
APPLICANT: Destroyer, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.

PRIOR FILING DATE: 1998-06-10 ;
; PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10 ;
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11 ;
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11 ;
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11 ;
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12 ;
; PRIOR APPLICATION NUMBER: 60/089440
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; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16 ;
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; PRIOR FILING DATE: 1998-06-19 ;
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; PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR FILING DATE: 1998-06-26 ;
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01 ;
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-06-26 ;
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01 ;
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02 ;
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02 ;
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02 ;
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07 ;
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07 ;
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09 ;

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MALLCIVLCLGQADIRTSLSITPEQMIEKAGETAYLPORCFTLGEPDQPLDIFWML 60
Db ||||| ||||| ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| :||| ||||| ||||| :|||
1 MALLCIVLCLGQADIRTSLSITPEQMIEKAGETAYLPORCFTLGEPDQPLDIFWML 60

Qy 61 PADNQKDQVILYSGDKIYDYQDKGRHFTSDUDKSGDASINVTNLQLSDIGTYQC 120
Db 61 PADNQKDQVILYSGDKIYDYQDKGRHFTSDUDKSGDASINVTNLQLSDIGTYQC 120

Qy 121 KYKKAPGVNKIKQTOLTKPSGTGTYVDSEBEIGNDPKLKCEPKGSPLYEWKLSN 180
Db 121 KYKKAPGVNKIKQTOLTKPSGTGTYVDSEBEIGNDPKLKCEPKGSPLYEWKLSN 180

Qy 181 SOKLPTMIAEMTSPVSYVKNSTEVGTSCTVKRNGSQCLRLDVPPSNRAGTIA 240
Db 181 SOKMPTSWLAEMTSSVSVKNSASSEYSGTYSCTVRNRVGSDOCLLRINVVPPSNKAGLIA 240

Qy 241 GAVIGVGLALVIGLIFCCR 261
Db 241 GAVIGVGLALVIGLIFCCR 261

RESULT 11
US-09-993-687-505
; Sequence 505, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspetr
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J.Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730P1C1

CURRENT APPLICATION NUMBER: US/09/993, 587

CURRENT FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088033

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088326

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088167

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088212

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088217

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088655

PRIOR APPLICATION NUMBER: 60/088858

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/088861

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/088824

PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088826

PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/089105

PRIOR FILING DATE: 1998-06-12

PRIOR APPLICATION NUMBER: 60/089140

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/088876

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/089512

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089514

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089532

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089600

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089653

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089599

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089900

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089907

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/089908

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/089947

PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: 60/089948

PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: 60/089952

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PRIOR APPLICATION NUMBER: 60/089946

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090252

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PRIOR APPLICATION NUMBER: 60/090254

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090349

PRIOR FILING DATE: 1998-06-23

PRIOR APPLICATION NUMBER: 60/090355

PRIOR FILING DATE: 1998-06-23

PRIOR APPLICATION NUMBER: 60/090429

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090431

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090435

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090444

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090445

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090472

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090535

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090697
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MAUUCFCVLLCGVADLTLSSLTTPPEQMTETAKGCTAYLPCRETFGLPDEQPDIEWHLIS 60
Db 1 MAUUCFCVLLCGVADLTLSSLTTPPEQMTETAKGCTAYLPCRETFGLPDEQPDIEWHLIS 60
Qy 61 PADNQKVQDQVILYSGDKLYDDYQDLKGRVRHFTSNDIKGDASINVNLQLSDIGTYQC 120
61 PADNQKVQDQVILYSGDKLYDDYQDLKGRVRHFTSNDIKGDASINVNLQLSDIGTYQC 120
Qy 121 KVVKAPGIVNKKQLITVLLKPSGTRCYUDSEEIENDRKLKCIPKEGSILPLVWQKLSN 180
Db 121 KVVKAPGIVNKKQLITVLLKPSGTRCYUDSEEIENDRKLKCIPKEGSILPLVWQKLSN 180
Qy 181 SQKLUPTMLAEMTSPPVISVSKNASTEYSGRYSCTVNRVGSDOCILRLDVPPRNRASTIA 240
181 SQKLUPTMLAEMTSPPVISVSKNASTEYSGRYSCTVNRVGSDOCILRLDVPPRNRASTIA 240
Qy 241 GAVTGVLALVGLIIFCCR 261
241 GAVTGVLALVGLIIFCCR 261
Db 241 GAVTGVLALVGLIIFCCR 261
241 GAVTGVLALVGLIIFCCR 261

RESULT 12
US-09-989-734-505
; Sequence 505, Application US/09989734
; Publication No. US20030035531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
APPLICANT: Boststein, David
APPLICANT: Deboynes, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gezelb, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J.Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: KijJavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2730P1C64
CURRENT APPLICATION NUMBER: US/09/989, 734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-15
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087105
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167

PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Freq. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MALLICPVLICLGVALDTSISITPEQMEKAKGETAYIFCRLGPGDQGPDIEMWLS
Db 1 MALLICPVLICLGVALDTSISITPEQMEKAKGETAYIFCRLGPGDQGPDIEMWLS 60
Qy 61 PADNOKVQDVQILYSGDKYDDYQDLKGSHVFTSNDLKGDSASINVNLQSLDIGTQC 120
Db 61 PADNOKVQDVQILYSGDKYDDYQDLKGSHVFTSNDLKGDSASINVNLQSLDIGTQC 120
Qy 121 KVKKAPGVGNKTIOLTVLLPSGTRCYVDSSEEIGNDFKLKCEPKREGSLPLLYWOKLSN 180

RESULT 14
US-09-993-667-505
; Sequence 505, Application US/09993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:
; APPLICANT: Aszkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Hong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Garlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Napir, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: PCT730PC4
; CURRENT APPLICATION NUMBER: US/09/993, 667
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827

Db 121 KVKKAPGVGNKTIOLTVLLPSGTRCYVDSSEEIGNDFKLKCEPKREGSLPLLYWOKLSN 180
Qy 181 SOKMPTSMIAEMTSSVSKVNSSESTGTYSCTVRNGSDOCILRANVVPSPNKAGLIA 240
Db 181 SOKMPTSMIAEMTSSVSKVNSSESTGTYSCTVRNGSDOCILRANVVPSPNKAGLIA 240
Qy 241 GAVIGVIALVULGLIFCCR 261
Db 241 GAITGTLALALIGLIFCCR 261

PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19

Query Match	91.1%	Score	1238	DB	9	Length	352
Best Local Similarity	89.3%	Pred. No.	2.3e-80				
Matches	233	Conservative	13	Mismatches	15	Indels	0
Gaps	0						

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08/10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:43:23 ; Search time 18 Seconds
 (without alignments)
 1393.949 Million cell updates/sec

Title: US-09-899-634C-2
 Perfect score: 1359
 Sequence: 1 MALLCFVLLCGVADLRLS... AVIGVLALVLVLIIFCCR 261

Scoring table: BLOSUM2

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR_73: *
 1: pir1: *
 2: pir2: *
 3: pir3: *
 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 JC7780
 coxsackie- and adenovirus receptor - bovine
 C.Species: Bos primigenius taurus (cattle)
 C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
 C;Accession: JC7780
 R-Thoelen, I.; Koyaers, E.; Lindberg, M.; van Ranst, M.
 Biochem. Biophys. Res. Commun. 288, 805-808, 2001
 A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor
 A;Reference number: JC7780
 A;Content: Liver
 A;Accession: JC7780
 A;Molecule type: mRNA
 A;Residues: 1-365 <THO>
 A;Cross-references: GB:AY033651
 C;Comment: This protein serves as the primary adenoviral attachment site on bovine cell

Query Match 93.5%; Score 1270; DB 2; Length 365;

Best Local Similarity 93.1%; Pred. No. 3e-90; Matches 242; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Description
 Qy 1 MALLCFVLLCGVADLRLSITPENOMEKARGETAVLPCFTTLGEDQGPDIEMLS 60
 1 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Db 1 MELLRFLLICGVADFTRGSLITPEQMEKAKGETAVLPCFTTLGEDQGPDIEMLS 60
 1 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Qy 61 PADNQKVQVILYSGKYYDQDKGRVHFTSNLKGDSASINTNLQSDIGYQC 120
 61 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Db 61 PADNQKVQVILYSGKYYDQDKGRVHFTSNLKGDSASINTNLQSDIGYQC 120
 61 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Qy 121 KVVKAPGVGNKKIQLTVLWKPSGTRCYVDGSSERIGNDFKLKECPKEGSPLIXEWQKLSN 180
 121 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Db 121 KVVKAPGVGNKKIQLTVLWKPSGTRCYVDGSSBEGNDPKLKCPKEGSPLIXEWQKLSN 180
 121 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Qy 181 SOKLPTMLAEMSPVSPVSKNASTEGYGTSCVKNVGSQDCLLRDVPPSNRAGTIA 240
 181 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Db 181 SOKLPTMLAEMSPVSPVSKNASTEGYGTSCVKNVGSQDCLLRDVPPSNRAGTIA 240
 181 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 Qy 241 GAVIGVLALVLVLIIFCCR 260
 241 ||||| :||||| :||||| :|||

Db 241 GAVIGVLALVLVLIIFCCR 260

RESULT 2
 S55749

Junctional adhesion molecule precursor - human
 N;Alternate names: Fil platelet antigen; platelet adhesion molecule PAM-1; platelet Fil
 C;Species: Homo sapiens (man)
 C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C;Accession: A59406; S55749
 R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;
 J. Immunol. 163, 553-557, 1999
 A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut

Result No.	Score	Query	Match Length	DB ID	Description
1	1270	93.5	365	2	coxsackie- and adenovirus receptor - bovine
2	196	14.4	299	2	junctional adhesio
3	159.5	11.7	4162	3	connectin/titin -
4	159	11.7	5175	2	hypothetical prote
5	159	11.7	5198	2	hemicentin precurs
6	154	11.3	309	2	B-Lymphocyte activ
7	151	11.1	7962	2	elastic titin - hu
8	144	10.6	526	2	butyrophilin - bov
9	143	10.5	483	2	hypothetical prote
10	139.5	10.3	1091	2	glial cell membran
11	136.5	10.0	518	2	poliovirus recepto
12	136.5	10.0	518	2	heparan sulfate pr
13	131	9.6	1323	2	connectin 3B - chi
14	129.5	9.5	4391	2	perlecan precursor
15	128	9.4	525	2	butyrophilin precu
16	127.5	9.4	344	2	neuroctrinin - rat
17	127.5	9.4	464	2	transmembrane carc
18	127	9.4	512	2	biliary glycoprote
19	127	9.3	509	2	SHP substrate-1 pr
20	127	9.3	513	2	SHP substrate-1 pr
21	127	9.3	513	2	irregular chiam
22	126	9.3	246	1	Cmylin P0 protein
23	124	9.1	1336	2	Fil-1 tyrosine kin
24	123.5	9.1	538	2	vascular cell adhe
25	123.5	9.1	2222	2	sdk protein - frui
26	122.5	9.0	647	2	vascular cell adhe
27	122.5	9.0	739	2	vascular cell adhe
28	122	9.0	584	2	hypothetical prote
29	121.5	8.9	738	2	platelet-endotheli

A; Reference number: A59406; MUID:99323940; PMID:10395639	Db 3591 -----PKDGNLISDH---KYKISFFNK---WSGKLTINAGEDSGEYTFEFKNS 3634
A; Accession: A59406	Qy 126 PGVGNKIQOLTV--LLKPGSGTRCYVQSEETCNDFLKURCEPKEGSPTPLVYEM---OKL 178
A; Status: preliminary	Db 3635 VGSQSCCTASLQLSDRIMPSFIRKLKETYQGLGSSAILECK-WGSPILVSHFDQEI 3693
A; Molecule type: DNA	Qy 179 SNSQKLIPTLWALMTSPVSKVASTEVY--GYSCTWKRNGSDQCLRLDV-VPPS 233
A; Residues: 1-299 <OZA> GB:ADD42050; NID:95326797; PIDN:ADD42050.1	Db 3694 TSGDK---YQATLTDNTCSLKVNGLOBDMDGIVSYCATNAGSDECSAFLSVREPPS 3747
A; Cross-references: R.Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.	
Biochem. J. 310, 155-162, 1995	
A; Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a	
A; Reference number: S56749; MUID:95374438; PMID:7646439	
A; Accession: S56749	
A; Molecule type: protein	
A; Residues: 28-49, 'X', 51-53, 62-73, 'E', 75-103; 123, 'F' 125-130; 'P' 159-170; 'T' 206, 'X'	
A; Note: the order of the peptides other than the amino terminus was not determined	
C; Genetics:	
A; Gene: JAM	
C; Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane	
F1-25; Domain: signal sequence #status predicted <SIG>	
F; 26-299/product: junctional adhesion molecule #status predicted <MAT>	
Query Match 14.4%; Score 196; DB 2; Length 299;	
Best local Similarity 25.9%; Pred. No. 9.7e-08;	
Matches 72; Conservative 44; Mismatches 108; Indels 54; Gaps 14;	
Qy 1 MALLICFVILGQAVDLTRSIITPEQMEKAKGFTAYLPICRFN---LGPDQGDLIEM 58	
Db 12 LCLFLIAILCSLA---LGSVTPVHSSEPEVTPENPVKPCAYSGFSSPR----VEWK 63	
Qy 59 LSPADNQKIVDQVILYLSGDKLYDDYQDLKGVRVHTSNDLKGASINTNLQLDIGY 118	
Db 64 FDQGDTTR---LVCYN-NKLTASY---EDRVTF---LPTGIFTKSVTR--EDTGQY 107	
Qy 119 OCKVKVAPG---VGNIKKIQLTFLWLKGSGTGRYVGDSEEEIGNDFKUKCEPKEGSPLLYEWQ 176	
Db 108 TCMVSEBGGNSYGEVKVKLVLVLPFSKPTWNIPSSATIGNRAVLTCESEQDSPSEYTFW 167	
Qy 177 K-----LSNSQKLUPTLWALMTSPVSKVASTEVY--GYSCTWKRNGSDQCLRLDV-VPPS 222	
Db 168 RDGIVMPTNPKSTRAFNSNVSYVLNPTGELVFDPLSASD---TGEYSEARNGYGTPM 222	
Qy 223 C-LIRLDVPPSNRAGTAGAVAVGIVLALLAVLVLIGLIF 258	
Db 223 TSNAVRMEAV--ERNVGIVVAA--VLVTLILLGLVF 255	
RESULT 3	
T42633 connectin/titin - chicken (fragment)	
C; Species: Gallus gallus (chicken)	
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000	
C; Accession: T42633	
R; Yamada, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.: Ma	
Biochem. Biophys. Res. Commun. 220, 160-164, 1996	
A; Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re	
A; Reference number: Z22221; MUID:96254045; PMID:8660363	
A; Accession: T42633	
A; Status: preliminary; translated from GB/EMBL/DDJB	
A; Molecule type: mRNA	
A; Residues: 1-4162 <YAJ>	
A; Cross-references: EMBL:D83390; NID:91513029; PTDN:BA11308.1; PID:91513030	
A; Experimental source: breast muscle	
C; Keywords: skeletal muscle	
Query Match 11.7%; Score 159.5; DB 2; Length 4162;	
Best local Similarity 25.6%; Pred. No. 0.0015; Indels 49; Gaps 11;	
Matches 61; Conservative 38; Mismatches 90;	
Qy 12 GVADLITRSISITPEQMEB---KAKGETAYLPICRFN---LGPDQGDLIEMLSPAINQ 65	
Db 3845 GVKELEMVMDLFPTPVVSKDNPALKGETITLFCNAGSNPYQQ---LKW----- 3892	
Qy 66 KVDOVILYLSGDKLYDDYQDLKGVRVHTSNDLKGASINTNLQLDIGYQCKV 122	
Db 3893 -----AKGGSLLFDSFGARISLK-----ARUDIPHKKTDGYTCQA 3932	
Qy 123 KKAPGVGNKIQOLTVLKGSGTGRYVGDSEEEIGNDFKUKCEPKEGSPLLYEWOKLNSQ 182	
Db 3933 LNAAGTSEASVSVDVLVPPEINRDGIBMSPL-----PAQOSSTL---QCLRK 3979	
Qy 183 KLPPL-WLAET-----SVTIVKNAESTEVYSGIVCTVNRVGSQCLRL 227	
Db 3980 PVFGMRWTLNGTALTHSTPGITVASDSTPIQINNNVSLDKGVYTCYAVNVAGSDNLWNV 4039	
Qy 228 DVV--PPSNRAGT---LAG--AVIGVLL 248	
Db 4040 DVVQAPVISNGGTRQVIGELAVIECLV 4067	
RESULT 5	
T4290 hemicentrin precursor - Caenorhabditis elegans	
C; Species: Caenorhabditis elegans	
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000	
C; Accession: T43290; T20993; T24734	

R. Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A:Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
A:Reference number: Z22396
A:Accession: T43290
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-15198 <VOG>
A:Cross-references: EMBL:AF074901; PIDN: AAC26792.1
R.Sulston, J
submitted to the EMBL Data Library, December 1994
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Reference number: Z19355
A:Accession: T20993
A:Cross-references: EMBL:X60958; PIDN: G50111; PID: 950112
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: EMBL:Z47068; PIDN: CAA87336.1; GSPDB:GN00028; CBSP:F15G9.4b
A:Experimental source: clone F15G9
R.Kershaw, J
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: EMBL:Z47070; PIDN: CAA87345.1; GSPDB:GN00028; CBSP:F15G9.4b
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F15G9.4b
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 105/3; 1184/3;
252/2; 2593/3; 269/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1
Query Match Score 159; DB 2; Length 5198;
Best Local Similarity 25.4%; Pred. No. 0.002; Matches 68; Conservative 32; Mismatches 92; Indels 76; Gaps 12;
Matches 65; Conservative 55; Mismatches 108; Indels 56; Gaps 13;
C:Keywords: alternative splicing
Query Match Score 154; DB 2; Length 309;
Best Local Similarity 22.9%; Pred. No. 0.00017; Matches 65; Conservative 55; Mismatches 108; Indels 56; Gaps 13;
Db 3845 GVKLELEMVLDVFIPPVVSVKSDNPKIALGETITLFCNASGNPFPQ----LKW----- 3892
QY 66 KVDQVILYSGDKYDD--YYQDQIKGRHFTSNDLKGDASTINVNQLSDIGTYQCKV 122
Db 3893 -----AKGGSLLFDSPDGARTISIKG-----ARUDIPHKKTDVGDYTCQA 3932
QY 123 KKAPGVGNKKIQLTIVLKPGTRCYVDGSEBEIGNDFKLKCEPKRGSLPLLYEWQKLNSQ 182
Db 3933 LNAAGTSEASVSVSVDVLVPEEINRDIDMSPL-----PAQQLSTI----QCLAGK 3979
QY 183 KLPPLT-WLAEMT-----SPVTKVNASTEYSGTYSCTVKNRVSESDQCLRL 227
Db 3980 PVPQMRWTGTLATHSTPGITVASDSTFQINNVLSDLKGVTCAENVAGSDNLMYNV 4039
QY 228 DWW--PRESNRAFT---ING--AVIGVLL 248
Db 4040 DVVOAPVINSNGGTQKVIEGELAVIECLV 4067

RESULT 6
149503 B-lymphocyte activation antigen 7 precursor - mouse
N:Alternative names: MBP-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; T49521
R.Seelvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38: 292-295; 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789; PMID:7686531
A:Accession: I49503
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

RESULT 6
149503 B-lymphocyte activation antigen 7 precursor - mouse
N:Alternative names: MBP-2
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I38346
C:Label: S; Kolmerer, B.
Science 270: 293-296; 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: I57430; MUID:96026330; PMID:7686978
A:Accession: I38346
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: EMBL:X90569; PIDN: G1017426; PIDN: CAA62189.1; PID: 91017427
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188940
A:Map position: 2q31-2q31
Query Match Score 151; DB 2; Length 7962;
Best Local Similarity 23.9%; Pred. No. 0.015; Matches 61; Conservative 31; Mismatches 77; Indels 86; Gaps 12;

RESULT 8

Query Match Score 144; DB 2; Length 526;
Best Local Similarity 23.4%; Pred. No. 0.0019; Mismatches 50; Indels 56; Gaps 13; Matches 67; Conservative 50; Mismatches 113; Indels 56; Gaps 13;

C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C.Accession: A37821

A.Reference number: A37821; MUID:9035441; PMID:2387867
A;Accession: A37821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-526 <JAC>
A;Cross-references: GB:M35551; NID:gi1763685; PIDN:AAB39766.1; PID:gi162773
C;Keywords: transmembrane protein

Query Match Score 144; DB 2; Length 526;
Best Local Similarity 23.4%; Pred. No. 0.0019; Mismatches 50; Indels 56; Gaps 13; Matches 67; Conservative 50; Mismatches 113; Indels 56; Gaps 13;

C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C.Accession: A37821

A.Reference number: A37821; MUID:9035441; PMID:2387867
A;Accession: A37821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-526 <JAC>
A;Cross-references: GB:M35551; NID:gi1763685; PIDN:AAB39766.1; PID:gi162773
C;Keywords: transmembrane protein

RESULT 9

Query Match Score 139.5; DB 2; Length 1091;
Best Local Similarity 24.0%; Pred. No. 0.01; Mismatches 106; Indels 31; Gaps 9; Matches 55; Conservative 37; Mismatches 106; Indels 31; Gaps 9;

TU7346 Hypothetical protein DKrzp58601624.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17346
R;Duesterhoeft, A.; Laufer, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, September 1999

RESULT 9

Query Match Score 139.5; DB 2; Length 1091;
Best Local Similarity 24.0%; Pred. No. 0.01; Mismatches 106; Indels 31; Gaps 9; Matches 55; Conservative 37; Mismatches 106; Indels 31; Gaps 9;

TU7346 Hypothetical protein DKrzp58601624.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17346
R;Duesterhoeft, A.; Laufer, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, September 1999

RESULT 10

Query Match Score 143; DB 2; Length 493;
Best Local Similarity 26.3%; Pred. No. 0.0021; Mismatches 80; Indels 4; Gaps 3; Matches 41; Conservative 31; Mismatches 80; Indels 4; Gaps 3;

A;Reference number: A58532; MUID:96394313; PMID:8798419
A;Accession: A58532
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1091 <SUZ>
A;Cross-references: GB:D78572; NID:gi1545806; PIDN:BA11416.1; PID:gi1545807
A;Cross-references: GB:D78572; NID:gi1545806; PIDN:BA11416.1; PID:gi1545807
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-terminal domain: proteoglycan amino-terminal homology <PAH>
C;Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH>
F;71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F;95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F;118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F;142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F;191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F;214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F;238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F;262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F;286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;440-465/Domain: proteoglycan carbohydrate-terminal homology <PCH>

Query Match Score 139.5; DB 2; Length 1091;
Best Local Similarity 24.0%; Pred. No. 0.01; Mismatches 106; Indels 31; Gaps 9; Matches 55; Conservative 37; Mismatches 106; Indels 31; Gaps 9;

Db 615 GTTARIECATGHNPO---IAW----OK----DGG---TDPARERRMV 652
Qy 94 TSNDLKGSGASINTVNLQSLDITYQCKVKKAGPGVGNKKIQLTVLKPSPGTRCYVDDGSEB 153
Db 653 MPDD---DVFF-ITDVKIDDGMYCTAONSAGSVSANSATIVLETPSLAVLEDRVT 707

QY 154 IGDIFKLKCEPKKGSLPLIYEWOKLNSQKLPTLWAEMTSPVIVKNASTEYSGTVCT 213
 C:Species: Homo sapiens (man)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C:Accession: JC4024
 R: Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr
 Gene 155, 261-265, 1995
 A>Title: Complementary DNA characterization and chromosomal localization of a human gene
 A:Reference number: JC4024; MUID:95237621; PMID:7721102
 A:Accession: JC4024
 A:Molecule type: mRNA
 A:Residues: 1-518 <LOP>
 A:Cross-references: EMBL:X76400; NID:9732795; PIDN:CAA53980.1; PID:9732796
 A:Gene: GDB:PVRR1
 A:Cross-references: GDB:583951
 A:Map position: 11q23.1-11q24
 C:Superfamily: polytropavirus receptor; immunoglobulin homology
 C:Keywords: Glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-518/Domain: polytropavirus receptor-related protein #status predicted <TM>
 F:35-67, 82-139, 287, 308, 319/Domain: transmembrane #status predicted <TM>
 Best Local Similarity 10.0%; Score 136.5; DB 2; Length 518;
 Matches 67; Conservative 50; Mismatches 86; Indels 159; Gaps 17;
 QY 34 GETAYLPCKRFTLGPDQGQLDIEWLILSADNQKVDOV-----ILYLS---GDK 78
 Db 44 GTDPVVLHCSFFA-----NPFLPSVKITQVWQKSTNGSKVNVALYNPSKGS 88
 QY 79 YDDYYQDLKGRVFTSNDKGIASINTNLQSLDGTYYQCKVKKAGVGNGRKIQ--LT 136
 Db 89 VLPARY----RERVEFLRPSFT--DGTLRLSRLEDEGVYICEFATFP-TGNRESQNLIT 141
 QY 137 VULKPGSGTRCYVQDSBEI---GNDPKL--KCEPKKGSLPLIYEWOKLNSQKLPTL 185
 Db 142 VMAKPTN--WIEGTOAVIRAKKGQDDKTVLWACTSANGKPPSVTWSMTRKGEARYPGD 198
 QY 186 -----TMLAEMTSPVIVKNASTEYSGTVCT 201
 Db 199 SGTPMAPVIVISRYLVFSRRAHQSLACIVNTYHMDRFKESELITINQYEPETVIEFGDN 258
 QY 202 -----ASTEY-----SGTVSCT 213
 Db 259 WYQMDVVKLTCKADANPPATEYHWTLINGSLPKGKVEAQRTLFFKGKPINSYLAGTYICE 318
 QY 214 VKNRPGSDOCLLRDWW-----PPSN--RAGIAGAVIG----VILAVLVLIGLIFC 259
 Db 319 ATNPBGTGSGQEVNITEFPYTPSPPEHGRAGBVPTAIIIGVAGSILLVLTIVGGIVWA 378
 QY 260 CR 261
 Db 379 LR 380

RESULT 12

S18252
 heparan sulfate proteoglycan - mouse
 N;Alternate names: perlecan
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

QY 154 IGDIFKLKCEPKKGSLPLIYEWOKLNSQKLPTLWAEMTSPVIVKNASTEYSGTVCT 213
 C:Accession: S18252; A31917; B31917; S66460
 R:Noonan, D.M.; Full, A.; Valentine, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; H
 J. Biol. Chem. 266, 22939-22947, 1991
 A>Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
 adhesion molecule.
 A:Reference number: S18252; MUID:92078153; PMID:1744087
 A:Accession: S18252
 A:Molecule type: mRNA
 A:Residues: 1-3707 <NO>
 A:Cross-references: EMBL:W77174; NID:9200295; PIDN:AAA39911.1; PID:9200296
 R:Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
 A>Title: Identification of cDNA clones encoding different domains of the basement membr
 A:Reference number: A492680; MUID:8903410; PMID:2972708
 A:Accession: A31917
 A:Molecule type: mRNA
 A:Residues: 94-1601 <NO>
 A:Cross-references: GDB:J04054; NID:9200252; PIDN:AAA39899.1; PID:9200253
 A:Accession: B31917
 A:Molecule type: mRNA
 A:Residues: 1870-2600 <NO>
 A:Cross-references: GDB:J04055; NID:9200300; PIDN:AAA39912.1; PID:9200301
 R:Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
 A>Title: Structural properties of recombinant domain III-3 of perlecan containing a glo
 A:Reference number: S66460; MUID:95377282; PMID:7649154
 A:Accession: S66460
 A:Molecule type: protein
 A:Residues: 1272-1274, X', 1276, X', 1278-1279 <SCH>
 C:Superfamily: LDL receptor ligand-binding repeat homology; BGP homology; laminin G rep
 C:Keywords: glycoprotein
 F:119-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:326-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:764-811/Domain: laminin-type EGFR-like homology <LEG>
 F:1159-1206/Domain: laminin-type EGFR-like homology <LEG7>
 F:1163-1610/Domain: laminin-type EGFR-like homology <EG7>
 F:3163-3198/Domain: BGP homology <BGP>
 F:3270-3323/Domain: laminin G repeat homology <LG2>
 F:3464-3492/Domain: EGFR homology <EGF7>
 F:1256, 1891, 2336, 2394, 2427/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 10.0%; Score 136.5; DB 2; Length 3707;
 Best Local Similarity 21.3%; Pred. No. 0.079;
 Matches 61; Conservative 38; Mismatches 102; Indels 85; Gaps 12;
 QY 20 LSITTPSQMIEKRAKGEGAYLPERFTGIPEDPQDPLDTEFWLISADNQKVQVILYSDKI 79
 Db 2346 ISIEPPSTVQ--QGOKSFCK--LHEGAMPKIVWKI--RDOELEDNVHISPNSSII 2398
 QY 80 -----YDDYY--QDI-----KGRVH-----FTSDLK 99
 Db 2399 TIVAPGATMEPTACVAVSNVYMAQSTVNLSTHGPPVIVSLSGPPVIVKMGKDITFCIS 2458
 QY 100 SGD-----ASINVNLQSLDGTYYQCKVKKAGVGNCRK 132
 Db 2459 SGEPRSPRWRTRLGIPIPVLPRMFLGLMSHAMLKIASVKPSDAGTYCQAONALGTAQKQ 2518
 QY 133 IOLTY--LLKSGSGTGYWDGSR--EIGNDFKLCEPKKGSLPLIYEWOKLNSQKLPTL 186
 Db 2519 VELVDTDTVAPGTPOVQEESBLTIBAHTATLHCS-ATGNPPTITHWSKU---RAPL 2573
 QY 187 LWAEMTSPVIVKNASTEYSGTVCT 232
 Db 2574 PWQRHRIGNTLVIPIRVAQODSGQYICNATNSAGTHEATIVLHVE 2619

RESULT 13

P0568
 connectin 3B - chicken (fragment)

N;Alternate names: Cn3B protein

C;Species: *Gallos gallus* (chicken)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C;Accession: PN0568
R;Miyazawa, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanazawa, N.; Nakuchi, Y.; Kimura, S.; Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993
A;Title: A novel domain sequence of connexin localized at the 1 band of skeletal muscle
A;Reference number: PN0568; MUID:93356802; PMID:8352787
A;Accession: FN0568
A;Cross-references: DDBJ:DI6541; NID:9391629; PID:d1004495; PID:9391630
A;Experimental source: skeletal muscle
C;Comment: This protein string-like single molecule spans from the Z line to the M line
Query Match 9.6%; Score 131; DB 2; Length 1323;
Best local Similarity 23.7%; Pred. No. 0.06; Mismatches 53; Conservative 31; MisMatches 90; Indels 50; Gaps 10;
Matches 53; Conserved 31; Mismatches 90; Indels 50; Gaps 10;
Qy 24 TPEQMIEKAGETAYLPCRFGLPBDQGPDIEWLSPADNQKVQDQVILYSGDKIYDD 83
Db 184 TPLBEPQWVQTVGDSASLQCOVAGTPE-----MIVSW-----YKGD----- 217
Qy 84 YQDLKG---RVHFTSNDLKSQGDAISINVNLQLSDIGTQQKVKKAPGNGKKIQJTV-- 137
Db 218 -TKRGTTATVKMHP----KNQVATLVPSQVDPSDGSYEYICKVENTVGATSSLITVQE 271
Qy 138 -LLKPSGSGTRCYVDSSEBEGNDFKLUKECPKESGLPLIYEWOK---LSNSQKLPTLWLAEM 192
Db 272 RKLPPSFTRKLRDVETVGLPVTFDC-GIAGSEPIEVSKFDNRVKDYNVHSTFDNV 330
Qy 193 TSPVSIKVKAESTEVSgtSYCTVKVORGV---SDQCLRLRDVPP 232
Db 331 A-ILQILKDQKSLMgQYTCTASNAIGTASSGGKLVLTECKTPP 372

RESULT 14

A8096

perlecan precursor - human

N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote

C;Species: *Homo sapiens* (man)

C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 05-Nov-1999

C;Accession: H38096; SI9256; SI9256; A41059; A40306; B33625; A41736

R;Murdoch, A. D.; Dodge, G.R.; Cohen, I.; Tuin, R.S.; Iozzo, R.V.

J. Biol. Chem. 267, 8544-8557, 1992

A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membra

A;Reference number: A38096; MUID:92235084; PMID:1569102

A;Accession: A38096

A;Molecule type: mRNA

A;Residues: 1-1331 <MUR>

A;Cross-references: GB:M85289; NID:gi184426; PIDN:AAA52700.1; PID:gi184427

R;Kallunki, P.; Tryggvason, K.

J. Cell Biol. 116, 559-571, 1992

A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro

tein adhesion molecules and epidermal growth factor.

A;Reference number: A41736; MUID:92112994; PMID:1730768

A;Accession: S19256

A;Molecule type: mRNA

A;Residues: 1-57,'D','59-434,'A','436,'FL','438-449,'Q','451-502,'A','503-792,'K','794-908,'R'

71-2979,'H','2981-2994,'C','2996-3167,'T','3169-3240,'R','3242-3426,'R,'3428-3631,'Q','3633-3

A;Cross-references: EMBL:X62515

A;Reference number: S77946

A;Accession: S77945

A;Molecule type: mRNA

A;Residues: 1-57,'D','59-434,'A','436,'FL','438-449,'Q','451-502,'A','503-792,'K','794-908,'R'

71-2979,'H','2981-2994,'C','2996-3167,'T','3169-3240,'R','3242-3426,'R,'3428-3631,'Q','3633-4

A;Cross-references: EMBL:X62515; NID:29469; PID:CA44371.1; PID:gi9470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestila, M.; Shows, T.B.; Tryggvason, K.

Genomics 11, 389-396, 1991

A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the 9

A;Reference number: A41059; MUID:92120660; PMID:1685141

Qy 130 NKKIQLTVLKPSTCVRDVGSEEIGNDFKLUKECPKESGLPLIYEWOKLSNSOKLPTLW 189

Db 3288 EATILHYESPPTVATTPEHASVQAGTIVOLC-LAICDPPLTQWSRVGSS--LP--GR 3342

Qy 190 AEMTSPVSKVAKSTEVSgtSYCTVKVORGVSDQCLRDVV-PPSNRAGT 238

C;Species: *Gallos gallus* (chicken)

C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999

C;Accession: PN0568

A;Residues: RT,892-908,'R',910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 <KA2>

A;Cross-references: GB:S76336; NID:9243370; PIDN:AB21121.1; PID:924371

R;Bodge, G.R.; Kovalsky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, Genomics 10, 673-680, 1991

A;Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellul...

A;Reference number: A40306; MUID:91365376; PMID:169749

A;Accession: A40306

A;Molecule type: mRNA

R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van de... J. Cell Biol. 109, 3199-3211, 1989

A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal antibodies

A;Reference number: A33625; MUID:90078352; PMID:2667294

A;Accession: B33625

A;Molecule type: protein

A;Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>

A;Accession: A33625

A;Molecule type: protein

A;Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>

A;Accession: B33625

A;Note: peptide potentially matches four different regions of sequence shown

C;Genetics:

A;Gene: GB:HSPG2

A;Cross-references: GDB:126372; OMIM:142461

A;Map position: 1p36.1-1p36.1

C;Superfamily: LDL receptor/ligand-binding repeat homology; EGF homology; laminin G repeat

C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrane

F;1-21/Domain: signal sequence #status Predicted <SIG>

F;22-4391/Domain: perlecan #status Predicted <MAT>

F;22-193/Domain: I <DOM1>

F;194-530/Domain: II <DOM2>

F;199-224/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F;311-1676/Domain: III <DOM3>

F;1159-1206/Domain: laminin-type EGF-like homology <LEG>

F;1561-1610/Domain: laminin-type EGF-like homology <EG7>

F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>

F;1677-3686/Domain: IV <DOM4>

F;2007-2034/Domain: V <DOM5>

F;3687-4391/Domain: VI <DOM6>

F;3845-3880/Domain: EGFR homology <EG1>

F;388-3921/Domain: EGFR homology <EG2>

F;3953-4106/Domain: laminin G repeat homology <LG2>

F;414-4175/Domain: EGF homology <EG2>

F;419-4151/Region: motor neuron attachment (L-R-E) motif

F;4299-4301/Region: motor neuron attachment (L-R-E) motif

F;65-71, 76/Binding site: heparan sulfate (Ser) (covalent) #status Predicted <TRM>

F;89-54, 175, 211, 302, 3105, 3219, 3780, 3936, 4068/Binding site: carbohydrate sulfate (Ser) (covalent) #status Predicted <TRM>

F;2995-3933-4179/Binding site: chondroitin sulfate (Ser) (covalent) #status Predicted <TRM>

F;147-415/Region: motor neuron attachment (L-R-E) motif

F;149-4151/Region: motor neuron attachment (L-R-E) motif

F;155-171/Region: motor neuron attachment (L-R-E) motif

F;171-187/Region: motor neuron attachment (L-R-E) motif

F;189-205/Region: motor neuron attachment (L-R-E) motif

F;211-227/Region: motor neuron attachment (L-R-E) motif

F;229-245/Region: motor neuron attachment (L-R-E) motif

F;247-263/Region: motor neuron attachment (L-R-E) motif

F;265-281/Region: motor neuron attachment (L-R-E) motif

F;283-300/Region: motor neuron attachment (L-R-E) motif

F;301-318/Region: motor neuron attachment (L-R-E) motif

F;319-336/Region: motor neuron attachment (L-R-E) motif

F;337-354/Region: motor neuron attachment (L-R-E) motif

F;355-372/Region: motor neuron attachment (L-R-E) motif

F;373-390/Region: motor neuron attachment (L-R-E) motif

F;391-408/Region: motor neuron attachment (L-R-E) motif

F;409-426/Region: motor neuron attachment (L-R-E) motif

F;427-444/Region: motor neuron attachment (L-R-E) motif

F;445-462/Region: motor neuron attachment (L-R-E) motif

F;463-480/Region: motor neuron attachment (L-R-E) motif

F;481-498/Region: motor neuron attachment (L-R-E) motif

F;499-516/Region: motor neuron attachment (L-R-E) motif

F;517-534/Region: motor neuron attachment (L-R-E) motif

F;535-552/Region: motor neuron attachment (L-R-E) motif

F;553-570/Region: motor neuron attachment (L-R-E) motif

F;571-588/Region: motor neuron attachment (L-R-E) motif

F;589-606/Region: motor neuron attachment (L-R-E) motif

F;607-624/Region: motor neuron attachment (L-R-E) motif

F;625-642/Region: motor neuron attachment (L-R-E) motif

F;643-660/Region: motor neuron attachment (L-R-E) motif

F;661-678/Region: motor neuron attachment (L-R-E) motif

F;679-696/Region: motor neuron attachment (L-R-E) motif

F;697-714/Region: motor neuron attachment (L-R-E) motif

F;715-732/Region: motor neuron attachment (L-R-E) motif

F;733-750/Region: motor neuron attachment (L-R-E) motif

F;751-768/Region: motor neuron attachment (L-R-E) motif

F;769-786/Region: motor neuron attachment (L-R-E) motif

F;787-804/Region: motor neuron attachment (L-R-E) motif

F;805-822/Region: motor neuron attachment (L-R-E) motif

F;823-840/Region: motor neuron attachment (L-R-E) motif

F;841-858/Region: motor neuron attachment (L-R-E) motif

F;859-876/Region: motor neuron attachment (L-R-E) motif

F;877-894/Region: motor neuron attachment (L-R-E) motif

F;895-912/Region: motor neuron attachment (L-R-E) motif

F;913-930/Region: motor neuron attachment (L-R-E) motif

F;931-948/Region: motor neuron attachment (L-R-E) motif

F;949-966/Region: motor neuron attachment (L-R-E) motif

F;967-984/Region: motor neuron attachment (L-R-E) motif

F;985-1002/Region: motor neuron attachment (L-R-E) motif

F;1003-1020/Region: motor neuron attachment (L-R-E) motif

F;1021-1038/Region: motor neuron attachment (L-R-E) motif

F;1039-1056/Region: motor neuron attachment (L-R-E) motif

F;1057-1074/Region: motor neuron attachment (L-R-E) motif

F;1075-1092/Region: motor neuron attachment (L-R-E) motif

F;1093-1110/Region: motor neuron attachment (L-R-E) motif

F;1111-1128/Region: motor neuron attachment (L-R-E) motif

F;1130-1147/Region: motor neuron attachment (L-R-E) motif

F;1148-1165/Region: motor neuron attachment (L-R-E) motif

F;1166-1183/Region: motor neuron attachment (L-R-E) motif

F;1184-1201/Region: motor neuron attachment (L-R-E) motif

F;1199-1216/Region: motor neuron attachment (L-R-E) motif

F;1217-1234/Region: motor neuron attachment (L-R-E) motif

F;1235-1252/Region: motor neuron attachment (L-R-E) motif

F;1253-1270/Region: motor neuron attachment (L-R-E) motif

F;1271-1288/Region: motor neuron attachment (L-R-E) motif

F;1289-1306/Region: motor neuron attachment (L-R-E) motif

F;1303-1320/Region: motor neuron attachment (L-R-E) motif

F;1327-1344/Region: motor neuron attachment (L-R-E) motif

F;1351-1368/Region: motor neuron attachment (L-R-E) motif

F;1375-1392/Region: motor neuron attachment (L-R-E) motif

F;1399-1416/Region: motor neuron attachment (L-R-E) motif

F;1423-1440/Region: motor neuron attachment (L-R-E) motif

F;1458-1475/Region: motor neuron attachment (L-R-E) motif

F;1483-1500/Region: motor neuron attachment (L-R-E) motif

F;1507-1524/Region: motor neuron attachment (L-R-E) motif

F;1531-1548/Region: motor neuron attachment (L-R-E) motif

F;1555-1572/Region: motor neuron attachment (L-R-E) motif

F;1579-1596/Region: motor neuron attachment (L-R-E) motif

F;1603-1620/Region: motor neuron attachment (L-R-E) motif

F;1627-1644/Region: motor neuron attachment (L-R-E) motif

F;1651-1668/Region: motor neuron attachment (L-R-E) motif

F;1675-1692/Region: motor neuron attachment (L-R-E) motif

F;1699-1716/Region: motor neuron attachment (L-R-E) motif

F;1723-1740/Region: motor neuron attachment (L-R-E) motif

F;1757-1774/Region: motor neuron attachment (L-R-E) motif

F;1781-1798/Region: motor neuron attachment (L-R-E) motif

F;1805-1822/Region: motor neuron attachment (L-R-E) motif

F;1839-1856/Region: motor neuron attachment (L-R-E) motif

F;1873-1890/Region: motor neuron attachment (L-R-E) motif

F;1907-1924/Region: motor neuron attachment (L-R-E) motif

F;1931-1948/Region: motor neuron attachment (L-R-E) motif

F;1955-1972/Region: motor neuron attachment (L-R-E) motif

F;1979-1996/Region: motor neuron attachment (L-R-E) motif

F;2005-2022/Region: motor neuron attachment (L-R-E) motif

F;2039-2056/Region: motor neuron attachment (L-R-E) motif

F;2073-2090/Region: motor neuron attachment (L-R-E) motif

F;2107-2124/Region: motor neuron attachment (L-R-E) motif

F;2131-2148/Region: motor neuron attachment (L-R-E) motif</p

Db 3343 ATARNELLHFERAAPEDSGRYCRVTKYGSAAEAFAQQLVQGPPCSLIPAT 3392

RESULT 15

St70587 butyrophilin precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C;Accession: St70587
 R;Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
 Biochim. Biophys. Acta 1306, 1-4, 1996
 A;Title: Cloning and sequence analysis of human butyrophilin reveals a potential receptor
 A;Reference number: St70587; MUID:96201696; PMID:8616164
 A;Accession: St70587
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-526 <TAY>
 A;Cross-references: EMBL:U39576; NID:91326082; PIDN: AAC50489.1; PID:91326083

Query Match	9 4%	Score 128;	DB 2;	Length 526;
Best Local Similarity	21.5%	Pred. No. 0.033;		
Matches	56;	Mismatches 107;	Indels 48;	Gaps 12;
QY	25 PEQMIEKAKGETAYLPCKRFTLGPDQGP-LDIEWL--LSPADNQKVDOIYLVSGDKIY 80			
Db	34 PPEPLAVVGEDAELPCR--LSPNASAEHLRMRKVKSPA-----VLVRHDGRQE 84			
QY	81 DDYFODLKGGRVHFISNDLXSGDASINVNTNLQLSDIGTYOCKVKKEAPGVNKKIQLVILK 140			
Db	85 AEQMPPEYGRATLYQDGIAKGVRALIRGURVSDDGETCFFRDGSEEBALVHLKV--A 142			
QY	141 PSGTRCYVDGSEEIGNDFLKLC-----EPKEGSLPLLYEWQKLNSOKLPTLWLAEMT 193			
Db	143 ALGSDPHISMQVQENGIECLECTEVGWYPHQ-----VQWRTSKGEKFPS-TTSRR 192			
QY	194 SP-----VISVKNSTEYSGTYSCTVKNRVGSQCLLRDVVP--PSNRAGTIA 240			
Db	193 NPDEBEGLIFTVAASVIRDISTK--NVSCYTIONLLGQEKKVEISIPASSLPRLTTPWIVA 249			
QY	241 GAVIGVLLAVLVLGHTIFCCR 261			
Db	250 VAVILMVGLGULTICSIFITWR 270			

Search completed: July 9, 2003, 12:45:54
 Job time : 20 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	1238	91.1	365	1 CXAR_HUMAN	P78110 homo sapien
2	1216	89.5	365	1 CXAR_MOUSE	P97792 mus musculu
3	351.5	25.9	319	1 A33_HUMAN	Q99795 homo sapien
4	196	14.4	299	1 JAM1_HUMAN	Q97624 homo sapien
5	181.5	13.4	298	1 JAM2_HUMAN	P57087 homo sapien
6	161.5	12.6	298	1 JAM1_BOVIN	Q9k566 bos taurus
7	161.5	11.9	300	1 JAM1_MOUSE	Q87792 mus musculu
8	154	11.3	306	1 CD80_MOUSE	P00619 mus musculu
9	144	10.6	526	1 BUTY_BOVIN	P18892 bos taurus
10	136.5	10.0	740	1 PEC1_PIG	Q95242 sus scrofa
11	136.5	10.0	3707	1 PGBM_MOUSE	Q05793 mus musculu
12	131.32	9.7	517	1 KILO_RAT	Q15223 homo sapien
13	131.5	9.7	348	1 PVR1_TIG	Q9z018 rattus norv
14	129.5	9.5	515	1 PGBM_HUMAN	Q99116 sus scrofa
15	128	9.5	4393	1 NTRI_RAT	Q98160 homo sapien
16	128	9.4	526	1 BUTY_HUMAN	Q13410 homo sapien
17	127.5	9.4	344	1 VCA1_HUMAN	Q62718 rattus norv
18	127.5	9.4	526	1 CBA1_HUMAN	P13618 homo sapien
19	127	9.3	764	1 IICR_DROME	Q08180 drosophila
20	126	9.3	246	1 MYP0_HEFR	P20328 heterodontu
21	125.5	9.2	727	1 PEC1_MOUSE	Q08481 mus musculu
22	124	9.1	1336	1 VGR1_RAT	P53767 rattus norv
23	122.5	9.0	739	1 VCA1_RAT	P19320 homo sapien
24	121	8.9	738	1 PVR1_MOUSE	P16284 homo sapien
25	120.5	8.9	515	1 C166_CARAU	Q91766 mus musculu
26	120.5	8.9	555	1 MOG_MOUSE	Q9304 carassius a
27	120	8.8	246	1 NCM2_HUMAN	Q61885 mus musculu
28	120	8.8	837	1 FAS2_DROME	Q15194 homo sapien
29	120	8.8	873	1 MOG_RAT	P34082 drosophila
30	119.5	8.8	245	1 PVR_HUMAN	Q63315 rattus norv
31	119.5	8.8	417	1 FGR2_DROME	P15151 homo sapien
32	119.5	8.8	1052	1 DSCA_HUMAN	Q99147 drosophila
33	119	8.8	2124	1 P07897 rattus norv	P04669 homo sapien

ALIGNMENTS

RESULT 1					
ID	CXAR_HUMAN	STANDARD;	PRT;	365 AA.	
AC	P78110; 000614;				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-adenovirus receptor) (HCAR) (CVB3 binding protein).				
GN	CXADR OR CAR				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID	9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-#97190109; PubMed=9036860;				
RA	Bergelson J.M., Cunningham J.A., Drogue G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.; "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5"; Science 275:1320-1323 (1997).				
RT					
RL					
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-#97250541; PubMed=9096397;				
RA	Tonko R.P., Xu R., Phillips L.; "HCAR and MCAR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses"; J. Virol. 71:3356 (1997).				
RT					
RL					
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-#20008750; PubMed=10543405;				
RA	Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A., Bowles N.E.; "Genomic organization and chromosomal localization of the human Coxsackievirus B adenovirus receptor gene.,"				
RT					
RL					
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Anderson C.W., Kileczawa J., Dunn J.J., Preimuth P.; "Sequence and expression of CXADR, the human gene for the Coxsackievirus and adenovirus receptor." Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.				
CC	-1- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-SUPERAMILY.				
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				

CC EMBL; Y07593; CA68868_1; -
 DR EMBL; U907116; AAC51234_1; -
 DR EMBL; AF169366; AAP05908_1; -
 DR EMBL; AF169360; AAP05908_1; JOINED.
 DR EMBL; AF169361; AAP05908_1; JOINED.
 DR EMBL; AF169362; AAP05908_1; JOINED.
 DR EMBL; AF169363; AAP05908_1; JOINED.
 DR EMBL; AF169364; AAP05908_1; JOINED.
 DR EMBL; AF169365; AAP05908_1; JOINED.
 DR Genew; HGNC: 2559; CXADR.
 MIM; 602621; -
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR PFam; PF0047; Ig_2.
 DR SMART; SM00410; Ig_Like_1.
 DR SMART; SM00408; IgC2_1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL. 1 19 POTENTIAL,
 COxsackievirus AND ADENOVIRUS RECEPTOR.
 FT DOMAIN. 20 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7E64 CRC64;

Query Match Score 91.1%; Score 1238; DB 1; Length 365;
 Best Local Similarity 89.3%; Pred. No. 5.7e-96; Indels 0; Gaps 0;
 Matches 233; Conservative 13; Mismatches 15; FT SIGNAL. 1
 FT CHAIN 20 365 POTENTIAL.
 COxsackievirus AND ADENOVIRUS RECEPTOR

Qy 1 MALLICFVLLCGVADLTSLTSITPEQMIRKAKGETAYLPFCRFTLGPGDQPLDIEWLIS 60
 Db 1 MALLICFVLLCGVVDIFARSLSITPEMMEKAKGETAYLPCKFTLSPBQPLDIEWLIS 60

Qy 61 PADNQKVDDQVITLYSGDKIYDDYQDLKGVRHFTSNDLKSQGDAINTVNLQLSDIGTYQC 120
 Db 61 PADNQKVDDQVITLYSGDKIYDDYQDLKGVRHFTSNDLKSQGDAINTVNLQLSDIGTYQC 120

Qy 121 KVKKAPGVNNKKIQTLVLLKPSGTRCYVDSSEEIGNDFLUKCEPKEGSPLLYEWQNSN 180
 Db 121 KVKKAPGVANKKKIHLVVLVKGPSGARYCVGDSEEIGSDFEKKCPEKEGSPLQYEWQKLD 180

Qy 181 SQKLPTLWLAEMTSPVIVRNASTRTSYGTYSCTVQRVGSDOCLRLDVPPSNRAGTIA 240
 Db 181 SQKMPTSWLAEMTSSVIVRNASSEYGTYSCTVNRVGSDCQCLRLVPPSNKAGLIA 240

Qy 241 GAVIGVLLALAVLIGHIFCCR 261
 Db 241 GAVIGVLLALAVLIGHIFCCR 261

RESULT 2
 CXAR_MOUSE ID CXAR_MOUSE STANDARD; PRT; 365 AA.
 AC P97792; 009052; PRT; 365 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
 GN CXADR OR CAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090; [1]

SEQUENCE FROM N.A.
 STRAIN=C57BL/6J; TISSUE=Liver;
 MEDLINE=971190109; PubMed=9036860;
 RX Begleison J.M., Cunningham J.A., Drogueut G.; Kurt-Jones E., Kurt-Jones E.,
 RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.,
 RT "Isolation of a common receptor for Coxsackie B viruses and
 RT adenoviruses 2 and 5.", Science 275:1320-1323 (1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97250541; PubMed=9096397;
 RX Begleison J.M., Krithivas A., Crowell R.L., Finberg R.W.;
 RA Tomko R.P., Xu R., Philipson L.,
 RT "mCAR and mCAR: the human and mouse cellular receptors for subgroup C
 adenoviruses and group B coxsackieviruses.", Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356 (1997).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC "The murine CAR homologue (mCAR) is a receptor for coxsackie B
 RT viruses and adenoviruses.",
 RT Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Y10320; CAA71368_1; -
 DR EMBL; U90715; AAC53148_1; -
 DR EMBL; Y11929; CAA72679_1; -
 DR MGPD; MG1:1201679; Cxadr.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00410; Ig_Like_1.
 DR SMART; SM00408; IgC2_1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL. 1 19 POTENTIAL.
 COxsackievirus AND ADENOVIRUS RECEPTOR
 FT CHAIN 20 365 HOMOLOG.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 20 237 POTENTIAL.
 FT TRANSMEM 238 258 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 259 365 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 340 365 VAAPNLNSRMGAEVPMIAQSKDGSIV -> FKYAKTDGIT
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 54454B52A3B2A2 CRC64;

Query Match Score 1216; DB 1; Length 365;
 Best Local Similarity 88.1%; Pred. No. 3.9e-94; Indels 0; Gaps 0;
 Matches 229; Conservative 15; Mismatches 16; FT SIGNAL. 1 19 POTENTIAL.
 COxsackievirus AND ADENOVIRUS RECEPTOR
 FT CHAIN 20 365 HOMOLOG.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 20 237 POTENTIAL.
 FT TRANSMEM 238 258 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 259 365 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 340 365 VAAPNLNSRMGAEVPMIAQSKDGSIV -> FKYAKTDGIT
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 54454B52A3B2A2 CRC64;

Query Match Score 89.5%; Score 1216; DB 1; Length 365;
 Best Local Similarity 88.1%; Pred. No. 3.9e-94; Indels 0; Gaps 0;
 Matches 229; Conservative 15; Mismatches 16; FT SIGNAL. 1 19 POTENTIAL.
 COxsackievirus AND ADENOVIRUS RECEPTOR
 FT CHAIN 20 365 HOMOLOG.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 20 237 POTENTIAL.
 FT TRANSMEM 238 258 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 259 365 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 340 365 VAAPNLNSRMGAEVPMIAQSKDGSIV -> FKYAKTDGIT
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 54454B52A3B2A2 CRC64;

Qy 1 MALLICFVLLCGVADLTSLTSITPEQMIRKAKGETAYLPFCRFTLGPGDQPLDIEWLIS 60
 Db 1 MALLICFVLLCGVFDIFARSLSITPEMMEKAKGETAYLPCKFTLSPBQPLDIEWLIS 60

Qy 61 PADNQKVDDQVITLYSGDKIYDDYQDLKGVRHFTSNDLKSQGDAINTVNLQLSDIGTYQC 120
 Db 61 PADNQKVDDQVITLYSGDKIYDDYQDLKGVRHFTSNDLKSQGDAINTVNLQLSDIGTYQC 120

Qy 121 KVKKAPGVNNKKIQTLVLLKPSGTRCYVDSSEEIGNDFLUKCEPKEGSPLLYEWQNSN 180
 Db 121 KVKKAPGVANKKKIHLVVLVKGPSGARYCVGDSEEIGSDFEKKCPEKEGSPLQYEWQKLD 180

Qy 181 SQKLPTLWLAEMTSPVIVRNASTRTSYGTYSCTVQRVGSDOCLRLDVPPSNRAGTIA 240
 Db 181 SQKMPTSWLAEMTSSVIVRNASSEYGTYSCTVNRVGSDCQCLRLVPPSNKAGLIA 240

Qy 241 GAVIGVLLALAVLIGHIFCCR 261
 Db 241 GAVIGVLLALAVLIGHIFCCR 261

RESULT 2
 CXAR_MOUSE ID CXAR_MOUSE STANDARD; PRT; 365 AA.
 AC P97792; 009052; PRT; 365 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
 GN CXADR OR CAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090; [1]

Db	61	PSDNQIVDQVILYSGDKIYDNYYPDLIKGRVHFTSNDVKSGDASINVNLQLSDIGTYQC	120	
QY	121	KVKAPGVGNKKIQITVLKPKSGTGYCVDSEETGNDFLKLCKPEKGSLPLVNEWQKLSN	180	
Db	121	KVKAPGVANKKELLTLYKPSGTRCPVGDSEEIGNDFLKLCKPEKGSLPLQEWQKLSN	180	
QY	181	SQKLPTLWIAEMTSPVSVKNAESTYGTYSCTVQRGSDOCLRLDVPPSNRAGTA	240	
Db	181	SQMTTPWIAEMTSPVSVKNAESTYGTYSCTVQRVSQCMRLDVPPSNRAGTA	240	
QY	241	GAVIGVLLALVLIGHIFCC	260	
Db	241	GAVIGTLLALVLIGHIFCC	260	
Db	241	GAVIGTLLALVLIGHIFCC	260	
RESULT 3				
A33_HUMAN	A33_HUMAN	STANDARD;	PRT;	319 AA.
ID	A33_HUMAN	STANDARD;	PRT;	319 AA.
AC	Q99759;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
GN	GPA33			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE:Colon carcinoma;			
RC	MEDLINE=97165045; PubMed=9012807;			
RA	Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J., Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C., Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice B.C., Burgess A.W.;			
RA	"The human A33 antigen is a transmembrane glycoprotein and a novel member of the immunoglobulin superfamily."			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:469-474 (1997).			
RN	[2]			
RP	POST-TRANSLATIONAL MODIFICATIONS.			
RX	MEDLINE=97396159; PubMed=9245713;			
RA	Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W., Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J., Simpson R.J.;			
RA	"Characterization of posttranslational modifications of human A33 antigen, a novel palmitoylated surface glycoprotein of human gastrointestinal epithelium."			
RT	RT			
RL	Biochem. Biophys. Res. Commun. 236:682-686 (1997).			
CC	-!- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL EPITHELIUM AND IN 95% OF COLON CANCERS.			
CC	-!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 K OF N-LINKED CARBOHYDRATE.			
CC	-!- PTM: PALMITOYLATED.			
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL; U79725; AAC50957.1; -.			
DR	Genw; HGNC:445; GPA33.			
DR	MIM: 602171; -.			
DR	InterPro; IPR03006; Ig_MHC.			
DR	InterPro; IPR03600; Ig_like.			
DR	Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,			
DR	-----			
DR	InterPro; IPR03596; Ig_V.			
DR	PFam; PF00047; Ig_2.			
DR	SMART; SM00410; Ig_like_1.			
KW	Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein; Transmembrane; Signal; Antigen.			
FT	CHAIN 1	21	CELL SURFACE A33 ANTIGEN.	
FT	DOMAIN 22	235	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 236	256	CYTOSOLIC (POTENTIAL).	
FT	DOMAIN 257	319	IG-LIKE V-TYPE DOMAIN.	
FT	DOMAIN 36	124	IG-LIKE C2-TYPE DOMAIN.	
FT	DOMAIN 139	229	POLY-CYS.	
FT	DOMAIN 258	261	POTENTIAL.	
FT	DISULFID 43	117	POTENTIAL.	
FT	DISULFID 146	222	POTENTIAL.	
FT	DISULFID 162	211	POTENTIAL.	
FT	CARBOHYD 112	112	N-LINKED (GLCNAC, .).	
FT	CARBOHYD 200	200	N-LINKED (GLCNAC, .).	
FT	CARBOHYD 223	223	N-LINKED (GLCNAC, .).	
SO	SEQUENCE 319 AD;	35632 MW;	9BFC7AAF5C2408E CRC64;	
Query Match	10 LCGVADLIRSLSTTPBOMIEKAKGETAYLPCKPFTLGPEBDQGPUDIEM--LISPADNQK 66	25.9%	Score 351.5; DB 1; Length 319;	
Best Local Similarity	34.1%	Pred. No. 3..9e-22;		
Matches	89; Conservative	53; Mismatches	96; Indels	23; Gaps 11;
Qy	10 LCGVADLIRSLSTTPBOMIEKAKGETAYLPCKPFTLGPEBDQGPUDIEM--LISPADNQK 66	25.9%	Score 351.5; DB 1; Length 319;	
Db	12 LCARVTVTDIAISVTPQDVLRASQKSYTLPCYHTSTSSRECL-IQMDKLIT---H 65	25.9%	Score 351.5; DB 1; Length 319;	
Qy	67 VDDQVILYSGDK-ITYDDYYQDLKGRYHTFSNDLKSQDASINTVNLQLSDIGTYQCKVTK 124	25.9%	Score 351.5; DB 1; Length 319;	
Db	66 TERVVWPFNSNKVYHGELEY--KRNVYI-SNNAEQSSASITDQLTMADNGTYBCSYSL 121	25.9%	Score 351.5; DB 1; Length 319;	
Qy	125 APGV-GNEK-1IQTIVLILPKPSGTRCYDVGSEEIGNDFLKLCKPEKGSLPLLYEWQKLS-N 180	25.9%	Score 351.5; DB 1; Length 319;	
Db	122 MSDILEGNTKSVRVLVLYPPSKPECGEGETIGNNIQLTCQSKEGSPTPQYSWKRYNIL 181	25.9%	Score 351.5; DB 1; Length 319;	
Qy	181 SQKPTLMIAEMTS-PVLSVKAESTYSGTYSTKVRVGSQDCLLRLDVPPSNRAGTI 239	25.9%	Score 351.5; DB 1; Length 319;	
Db	182 NQOBP--LAQPASQGPYSLKNISTDSGYYICTSSNEEGTQFCNITVAVRSPSMVNTLY 238	25.9%	Score 351.5; DB 1; Length 319;	
Qy	240 AGAVIGVLLALVLLGLIIFCC 260	25.9%	Score 351.5; DB 1; Length 319;	
Db	239 VGIAGVVAALIIGIIYCC 259	25.9%	Score 351.5; DB 1; Length 319;	
RESULT 4				
JAM1_HUMAN	JAM1_HUMAN	STANDARD;	PRT;	299 AA.
ID	JAM1_HUMAN	Q91624;		
AC		AC		
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11 receptor).			
GN	JAM1 OR JCAM			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:99322940; PubMed:10395639;			
RA	Ozaki H., Ishii K., Horiechi H., Arai H., Kawamoto T., Okawa K., Iwamatsu A., Kita T.;			
RA	"Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";			
RT	J. Immunol. 163:553-557 (1999).			
RL	J. Immunol. 163:553-557 (1999).			
RN	J. Immunol. 163:553-557 (1999).			
RP	SEQUENCE FROM N.A.			
RA	Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,			

Kornecki E., cloning and sequencing of the cDNA of F11 receptor, a novel Ig superfamily member from human platelets"; Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 [3]

SEQUENCE FROM N.A.

Naik U.P., DeLeon P., Spychala J.; "Cloning and characterization of PAM-1, a novel platelet adhesion molecule involved in platelet activation"; Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 [4]

SEQUENCE FROM N.A.

TISSUE=Brain;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassnerhuber J., Glassl S., Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N., Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambut R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs"; Genome Res. 11:422-435 (2001).
 CC -!- FUNCTION: PLAYS A ROLE IN REGULATING MONOCYTE TRANSMIGRATION
 CC INVOLVED IN INTEGRITY OF EPITHELIAL BARRIER. INVOLVED IN PLATELET ACTIVATION.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH EPITHELIAL AND ENDOTHELIAL CELLS.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.

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CC DR AF111713; ADD42050_1;
 EMBL AF207907; AA122829_1;
 DR AF172398; ADD48877_1;
 EMBL AL136649; CAB66584_1;
 DR MIM:605721; -;
 DR InterPro:IPR03006; IG_MHC.
 DR InterPro:IPR003600; IG_Like.
 DR InterPro:IPR003596; IG_V.
 DR Pfam:PF00047; ig_2;
 DR SMART:SM00410; IG_Like_1.
 DR SMART:SM00406; IGv_1.
 KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal

FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 299 JUNCTIONAL ADHESION MOLECULE 1.
 FT DOMAIN 26 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 259 POTENTIAL.

FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 116 IG-LIKE V-TYPE DOMAIN 1.
 FT DOMAIN 146 219 IG-LIKE V-TYPE DOMAIN 2.
 FT DISULFID 50 109 POTENTIAL.

FT DISULFID 153 212 POTENTIAL.
 FT CARBOHYD 185 185 N-LINKED (GLCNAC, .) (POTENTIAL).
 SEQUENCE 299 AA; 32583 MW; D95DE2FFEA23D2851 CRC64;

Query Match 14.4%; Score 196; DB 1; Length 299;
 Best Local Similarity 25.9%; Pred. No. 3_3e-09;
 Matches 72; Conservative 44; Mismatches 108; Indels 54; Gaps 14;

QY 1 MALLICFVJLJCGVADLTSRSITTEQMIKEKGETAYLPCRF--LGIEDQGQLDIDML 58
 DB 12 LCLFLIAILCSLA--LGSTVTHSSEPEVIREPPNNPVKLSCAYSGFSSPR----VWK 63

Qy 59 LSPADNQKVQDVITLILYSSCDKIVDDYYQDLKGGRVHTFTSNDLKSGDASINVNLQLSDIGTY 118
 Db 64 FDQGDTTR---IYCYN-NKTAZY---EDVTF---LPRTCTFSVTR---EDVTCY 107
 RN 119 QCKVKAPG--VGNKCIQTLVLLKPSGTRCYDGEETGNDPFLKCBPKEGSLPLLYEWQ 176
 Db 108 TCMVSEEGNSYGEVKVLIVLVPSPSKPTVNIPSATGNRAVLTCEQDGSPSETWFL 167
 177 K-----LSNSQKLPTWLAEMTSPPVSYKNASTEYSGYSCTYKRNVRGSDQ 222
 Db 168 KDGIVMPTNPKSTRAFNSSYLNPTGELVDPLSASD----TGEYSCEARNGYCPTM 222
 RP 223 C--LLRLDVPPSNRAGTAGAVGIVLLAVLGLLIF 258
 Db 223 TSNAVREAV--ERNGVIVAA--LVLTLLGILVF 255
 RESULT 5
 JAM2_HUMAN
 ID JAM2_HUMAN STANDARD; PRT; 298 AA.
 AC P57087;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Junctional adhesion molecule 2 precursor (vascular endothelial junction-associated molecule) (VE-JAM).
 GN JAM2 OR VEJAM OR C21orf43.
 OS Homo sapiens (Human).
 OC Marmosita; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Teleostei; Euteleostomi; Homo.OC
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN 11 J. Biol. Chem. 275:19139-19145 (2000).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vascular endothelial cells;
 RX MEDLINE=10779514; PubMed=10779514;
 RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.; "Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells"; J. Biol. Chem. 275:19139-19145 (2000).
 RN 12 J. Biol. Chem. 275:19139-19145 (2000).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=20501930; PubMed=10945976;
 RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerke R.J., Vanderslice P., Morris A.P., Brock T.A.; "A novel protein with homology to the junctional adhesion molecule"; Characterization of leukocyte interactions"; J. Biol. Chem. 275:34750-34756 (2000).
 RN 13 J. Biol. Chem. 275:34750-34756 (2000).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Straubberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIJA OF OTHER VESSELS. LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL CELLS.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- DATABASE: NAME=PROW; NOTE=PRO 2.1-3 (2001); WWW="http://www.ncbi.nlm.nih.gov/prow Guide/1652492186_g.htm".
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or send an email to license@isb-sib.ch).

CC	redistribution of junctional adhesion molecule in human endothelial cells ";
DR	EMBL; APF55910; AAH81223.1; -.
DR	EMBL; AY016009; AAC49022.1; -.
DR	EMBL; BCO17779; AAH17779.1; -.
DR	Genew; HGNC:1468; JAM2.
DR	MIM; 606870; -.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003598; Ig_C2.
DR	Pfam; PF00047; Ig_2.
DR	SMART; SM00410; IgE2; 1.
KW	Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT SIGNAL	20 POTENTIAL; ADHESION MOLECULE 2.
FT CHAIN	21 298 EXTRACELLULAR (POTENTIAL).
FT DOMAIN	21 238 POTENTIAL.
FT TRANSMEM	239 259 CYTOPLASMIC (POTENTIAL).
FT DOMAIN	260 298 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN	43 116 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN	148 221 POTENTIAL.
FT DISULFID	50 109 POTENTIAL.
FT DISULFID	155 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	298 AA; 33207 MW; CA78E18E22DCAE CRC64;
Query Match	13.4% Score 181.5; DB 1; Length 298;
Best Local Similarity	24.0% Pred. No. 5.4e-08;
Matches	67; Conservatory 44; Mismatches 115; Indels 53; Gaps 10;
Qy	1 MAIILCFVLLCGAVDLTSSLITTEDEQMIKAKGETAYLPCCRFLIGPQDGQLDIEWLIS 60
Db	10 LLLRLRYVVALGYHKAYGSAPKDQQVTFAVEQBAALLACK---TPKTVTSSPLEW--- 63
Qy	61 PADNOKVDQVTLIYSGDKIYDDYO---DLKGRRHFTSNDLKSGDAStINVTNLQLSDI 115
Db	64 ---KKL-----GRSVSFVYYQQTOLQGDFKQRAEMI-----DFNIRIQKVTRSDA 104
Qy	116 GTYQCKVKKKPAVGNGKKIQ----LTVLLKPKSGTRCYDGSEEIGNDFLKCKBEGKLSP 170
Db	105 GKYRCBV-SAPSEQCNLIEDDTVTLEVLYAPAVBCEVPSSALSGTVWLRCQDKEGNPA 163
Qy	171 LLYEHQK---LSN---SQKLPLTIWLAEMTSPVSKRNASTEYSGTStCTVKNRVGD 221
Db	164 PEYTWFKGIRLLENPRPLGSQSTNSSYNTKTGTLQFNTVSKLDTGEYSCEARNVSGYR 223
Qy	222 QCLLRUDVPPSNRAGTIAGAVIGVLLALVLIGLIIFC 260
Db	224 RC-----PGKRMQDDLNISGIIAIAVVVALVISVC 254
RESULT 6	JAM1_BOVIN STANDARD; PRT; 298 AA.
ID	JAM1_BOVIN STANDARD; PRT; 298 AA.
AC	Q9XT56;
AC	Q9XT56; (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
JM	JAM1.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomia;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Medline=932390; PubMed=1035639;
RA	Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA	Iwanatsu A., Kitai T.;
	"Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes
RT	cells ";
RL	J. Immunol. 163:553-557(1999).
CC	-1. FUNCTION PLAYS A ROLE IN REGULATING MONOCYTE TRANSMIGRATION INVOLVED IN PLATELET ACTIVATION (BY SIMILARITY).
CC	-1. SUBCELLULAR LOCATION: TYPE I membrane protein (Potential).
CC	-1. TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH EPITHELIAL AND ENDOTHELIAL CELLS.
CC	-1. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC	-1. SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC	-- SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
CC	-- EMBL; AE11714; ADD42051.1; -.
DR	InterPro; IPRO03006; Ig_MHC.
DR	InterPro; IPRO03528; Ig_C2.
DR	InterPro; IPRO03600; Ig_Like.
DR	SMART; SM00410; IgE2; 1.
DR	SMART; SM00408; IgC2; 1.
KW	Tight Junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW	Repeat; Signal; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW	Repetitve; Signal; Immunoglobulin domain; Glycoprotein; Transmembrane;
FT SIGNAL	20 POTENTIAL.
FT CHAIN	21 298 EXTRACELLULAR (POTENTIAL).
FT DOMAIN	21 238 POTENTIAL.
FT TRANSMEM	239 259 CYTOPLASMIC (POTENTIAL).
FT DOMAIN	260 298 IG-LIKE V-TYPE DOMAIN.
FT DISULFID	43 116 IG-LIKE C2-TYPE DOMAIN.
FT CARBOHYD	148 221 POTENTIAL.
FT DISULFID	50 109 POTENTIAL.
FT CARBOHYD	155 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	298 AA; 33207 MW; CA78E18E22DCAE CRC64;
Query Match	13.4% Score 181.5; DB 1; Length 298;
Best Local Similarity	24.0% Pred. No. 5.4e-08;
Matches	67; Conservatory 44; Mismatches 115; Indels 53; Gaps 10;
Qy	1 MAIILCFVLLCGAVDLTSSLITTEDEQMIKAKGETAYLPCCRFLIGPQDGQLDIEWLIS 60
Db	10 LLLRLRYVVALGYHKAYGSAPKDQQVTFAVEQBAALLACK---TPKTVTSSPLEW--- 63
Qy	61 PADNOKVDQVTLIYSGDKIYDDYO---DLKGRRHFTSNDLKSGDAStINVTNLQLSDI 115
Db	64 ---KKL-----GRSVSFVYYQQTOLQGDFKQRAEMI-----DFNIRIQKVTRSDA 104
Qy	116 GTYQCKVKKKPAVGNGKKIQ----LTVLLKPKSGTRCYDGSEEIGNDFLKCKBEGKLSP 170
Db	105 GKYRCBV-SAPSEQCNLIEDDTVTLEVLYAPAVBCEVPSSALSGTVWLRCQDKEGNPA 163
Qy	171 LLYEHQK---LSN---SQKLPLTIWLAEMTSPVSKRNASTEYSGTStCTVKNRVGD 221
Db	164 PEYTWFKGIRLLENPRPLGSQSTNSSYNTKTGTLQFNTVSKLDTGEYSCEARNVSGYR 223
Qy	222 QCLLRUDVPPSNRAGTIAGAVIGVLLALVLIGLIIFC 260
Db	224 RC-----PGKRMQDDLNISGIIAIAVVVALVISVC 254
RESULT 7	JAM1_MOUSE STANDARD; PRT; 300 AA.
ID	JAM1_MOUSE STANDARD; PRT; 300 AA.
AC	Q87792;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 41, Last annotation update)
JM	JAM1.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomia;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Medline=932390; PubMed=1035639;
RA	Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA	Iwanatsu A., Kitai T.;
	"Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes

InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 37 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN 38 306 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 38 246 POTENTIAL.
FT TRANSMEM 267 268 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 269 306 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 47 126 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 158 226 IG-HINGE LIKE (POTENTIAL).
FT DOMAIN 227 246 POTENTIAL.
FT DISULFID 54 119 POTENTIAL.
FT CARBOHYD 165 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 306 AA; 34589 MW; 1DEADE031B84C62 CRC64;
CC 11.3% Score 154; DB 1; Length 306;
CC Best Local Similarity 22.9%; Pred. No. 1..e-05;
CC Matches 65; Conservative 55; Mismatches 108; Indels 56; Gaps 13;
CC 3 LLLCPVLLCGVADLTRLSSITTPQEMIEKAKGETAYLPICRFETLGPDQQLDIELWLLSPA 62
Db 21 LLLFVFLRLSQQSSDV----DQQLSKSVKDVKLPPCRYNPSHEDSBDRITYW---- 70
CC DNOKUDQVII-LYSGD-KIYDDY-QDLKGVRHFTNSDLKSGDASINTNLQLSDIGTYQC 120
Db 71 -QKHDKVVLSSIASKLKVWEY---KORTLYDNTT---SLILIGVLSRGTSC 119
CC 121 KVKAAPGVMRKIQUTVLLKPS----GTRCYVDGSEETGNDKFLKCBPREGSPLLYEW 175
Db 120 VVQKKER-GTYEVKHLALVLSIKADFSTPNITEGGNPSADTRKRTCPASGGFPKPKPFSW 178
CC 176 QKLNSNSQKLPLTMLAEMTSPVISVKNST--EYSGTYSCTVKNRVGSDQCLLRL---- 227
Db 179 --LENGRELPQINTTISQDPESELTTISSOLDNFNTNTRITK-----CLIKYGDAAVS 229
CC 228 -----DVVPPSNRAGTIAVGIVLLALVLLIGLIFC-CR 261
Db 230 EDFTWKEKPPEDPDPSKNTLVIFGAGFAVTVVVVTKCFCK 273

RESULT 9
BUTY_BOVIN
ID BUTY_BOVIN STANDARD; PRT; 526 AA.
AC P18832; Q18955; O18959;
DT 01-NOV-1990 (Rel. 16, Created)
DT 16-OCT-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Butyrophilin precursor (BT).
GN BTNA1 or BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Buthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
NCBI_TAXID:9913;
RN SEQUENCE FROM N.A. AND SEQUENCE OF 27-47.
RN MEDLINE=9035441; PubMed=2387867;
RA Jack L.J.W.; Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein expressed in mammary tissue and secreted in association with the milk-fat globule membrane during lactation.", J. Biol. Chem. 265:14481-14486 (1990).
RN [2] SEQUENCE FROM N.A.

Query Match 10.6%; Score 144; DB 1; Length 526;
Best Local Similarity 22.4%; Pred. No. 0.0015; Gaps 10;
Matches 63; Conservative 51; Mismatches 121; Indels 46; Gaps 10;

Qy 4 LLCHVLLCGVADLTRLSSITTPQEMIEKAKGETAYLPICRFETLGPDQQLDIELWLL--LS 60
Db 13 LLITILLQPLKLDSSAPPDVIGQEPILAVGEADPCLRSLPSVNSAKG-MELRWFRRVKS 71
Qy 61 PADNQKVHDQVYIISQD1KYYDDYQD1KGRVHTTSND1KSGDASINTNLQLSDIGTYQC 120
Db 72 PA-----VFVSRSEQOBGBEMAEYFRGRVSLVEDHIAEGSVAVRIQEVKASDGEYRC 124

RESULT 10
 PECL_PIG STANDARD; PRT; 740 AA.
 AC Q95242;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Platelet endorphin cell adhesion molecule precursor (PECAM-1)
 DB (CD11 antigen).
 GN PECAM1
 OS Sus scrofa (Pig)
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TAXID=9823;
 RN [1]
 RA Nasu K.
 RL Submitted (NOV 1996) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE EXPRESSED ON
 CC PLATELETS AND AT ENDOTHELIAL CELL INTERCELLULAR JUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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SMART; SM00409; IG_2; SMART; SM00410; IG_like_1.
 DR X98505; CAA67129.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_like.
 DR PF00047; Ig_4.
 DR SMART; SM00409; IG_2.
 KW Immunoglobulin domain; Glycoprotein; Cell adhesion; Transmembrane;
 KW Repeat; Signal; BY SIMILARITY.
 FT SIGNAL 1 27
 FT CHAIN 28 740 BY SIMILARITY.
 FT DOMAIN .28 602 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 603 621 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 622 740 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 50 116 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 145 213 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 249 311 IG-LIKE C2-TYPE DOMAIN 4.
 FT DOMAIN 340 394 IG-LIKE C2-TYPE DOMAIN 5.
 FT DOMAIN 425 484 IG-LIKE C2-TYPE DOMAIN 6.
 FT DISULFID 517 580 POTENTIAL.
 FT DISULFID 57 109 POTENTIAL.
 FT DISULFID 152 206 POTENTIAL.
 FT DISULFID 256 304 POTENTIAL.
 FT DISULFID 347 387 POTENTIAL.
 FT DISULFID 432 477 POTENTIAL.
 FT DISULFID 524 573 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 52 552 SQ SEQUENCE 740 AA; F312DC62C4B4A217 CRC64;

Query Match 10.0%; Score 136.5; DB 1; Length 740;
 Best Local Similarity 26.0%; Pred. No. 0.00094;
 Matches 47; Conservative 36; Mismatches 85; Indels 13; Gaps 6;
 Query 84 YQDLKGRVHTFTSDLKGDDASINTNQLSDIGTYQC--KVKKAPGVGNKIKTQITWLK 140
 Db 443 YQDLKGSPLLAQNVSNEPAFKDN-PTKDV-EYQCTADNCHSHAGMPSKYLRKVITAP 500
 Query 141 PSSTRCYVDGSEB1--GNDFLKUCPKPEKGSPLPLIYEQKLNSQKLPTLWIAEMTSPVIS 198
 Db 501 VEEVKLSSLSEVESSOAVIQLCSVKEGSPTTYKEKVKPFHQVTUND-TQAIWH 559
 Query 199 VKNASTEYSGTYSCTVKNRVGSDDQLLRLDVVP----PSNRAGTAGAVICVLALVLI 253
 Db 560 KPKASKDQGQYCLASRNATPSKFNQSLNLLAVRVYLAPWKGLIAVVIAVIAVILL 619
 Query 254 G 254
 Db 620 G 620

RESULT 11
 PGBM_MOUSE STANDARD; PRT; 3707 AA.
 AC Q05793;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSFG) (Perlecan) (PLC).
 GN HSFG2.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RP SEQUENCE FROM N.A.;
 RC TISSUE:Melanoma;
 RX MEDLINE:901078153; PubMed=1744087;
 RA Noonan D.M., Fullie A., Valente P., Cai S., Horigan E., Sasaki M.,
 RA Yamada Y., Hassell J.R.;
 RA "The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion molecule.";
 RT J. Biol. Chem. 266:22233-22239 (1991).
 RL [2]
 RN SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE:89034110; PubMed=2772708;
 RX Noonan D.M., Horigan E.A., Ledbetter S.R., Vogel G., Sasaki M.,
 RA Yamada Y., Hassell J.R.;
 RA "Identification of cDNA clones encoding different domains of the basement membrane heparan sulfate proteoglycan.";
 RT J. Biol. Chem. 263:16379-16387 (1988).
 CC -!- FUNCTION: This protein is an integral component of basement membrane proteoglycan. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.
 CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type IV.

CC -|- SUBCELLULAR LOCATION: Extracellular.
 CC -|- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES .
 CC -|- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
 CC AND O-LINKED OLIGOSACCHARIDES .
 CC -|- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS .
 CC -|- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS .
 CC -|- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV .
 CC -|- SIMILARITY: CONTAINS 15 IMMUNOGLOBULIN C2-TYPE DOMAINS .
 CC -|- SIMILARITY: CONTAINS LAMININ G-LIKE DOMAINS .
 CC -|- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN .
 CC -|- SIMILARITY: CONTAINS 1 SEA DOMAIN .

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CC EMBL; M77174; AAA3991.1; .
 DR EMBL; J04054; AAA39899.1; .
 DR HSSP; P01130; IAUU .
 DR MGDB; MGI_96257; HSP92 .
 DR InterPro; IPR000561; EGF-like .
 DR InterPro; IPR000742; EGF_2 .
 DR InterPro; IPR001438; EGF_I .
 DR InterPro; IPR003006; Ig_MHC .
 DR InterPro; IPR00598; Ig_C2 .
 DR InterPro; IPR002172; LDL_recept_A .
 DR InterPro; IPR000034; Laminin_B .
 DR InterPro; IPR000049; Laminin_BGF .
 DR InterPro; IPR001791; Laminin_G .
 DR InterPro; IPR000082; SEA_domain .
 DR Pfam; PF00008; EGF ; 4 .
 DR Pfam; PF00047; Ig ; 15 .
 DR Pfam; PF00052; laminin_B ; 3 .
 DR Pfam; PF00053; laminin_G ; 8 .
 DR Pfam; PF00054; laminin_G ; 3 .
 DR Pfam; PF00057; ldl_recept_a ; 4 .
 DR Pfam; PF01390; SEA ; 1 .
 DR Prodom; PR00010; EGFBLOOD .
 DR Prodom; PD003031; Laminin_B ; 3 .
 SMART; SM00180; EGF_Lam; 7 .
 SMART; SM00001; EGF_like ; 6 .
 SMART; SM00408; IgG2 ; 14 .
 SMART; SM00192; IgD ; 4 .
 SMART; SM00281; LambB ; 3 .
 SMART; SM00282; Lang ; 3 .
 SMART; SM00200; SEA ; 1 .
 PROSITE; PS00022; EGF_1 ; 8 .
 PROSITE; PS01186; EGF_2 ; 5 .
 PROSITE; PS01248; LAMININ_TYPE_EGF ; 11 .
 PROSITE; PS01209; LDLRA_1 ; 4 .
 PROSITE; PS50066; LDLRA_2 ; 4 .
 DR Signal; Basement_membrane; Proteoglycan; Repeat; Glycoprotein;
 KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
 Extracellular matrix; EGF-like domain .
 SIGNAL 1 21 POTENTIAL
 CHAIN 22 3707 BASEMENT MEMBRANE-SPECIFIC HEPARAN
 SULFATE PROTEOGLYCAN CORE PROTEIN .
 FT DOMAIN 80 194 SEA .
 FT DOMAIN 195 234 LDL-RECEPTOR CLASS A 1 .
 FT DOMAIN 281 319 LDL-RECEPTOR CLASS A 2 .
 FT DOMAIN 320 359 LDL-RECEPTOR CLASS A 3 .
 FT DOMAIN 360 403 LDL-RECEPTOR CLASS A 4 .
 FT DOMAIN 404 504 Ig-LIKE C2-TYPE DOMAIN 1 .
 FT DOMAIN 521 530 LAMININ EGF-LIKE 1 (N-TERMINAL) .
 FT DOMAIN 531 730 LAMININ DOMAIN IV 1 (DOMAIN III A) .
 FT DOMAIN 731 763 LAMININ EGF-LIKE 1 (C-TERMINAL) .

FT DOMAIN 764 813 LAMININ EGF-LIKE 2 .
 FT DOMAIN 814 871 LAMININ EGF-LIKE 3 .
 FT DOMAIN 879 923 LAMININ EGF-LIKE 4 (INCOMPLETE) .
 FT DOMAIN 924 933 LAMININ EGF-LIKE 5 (N-TERMINAL) .
 FT DOMAIN 934 1125 LAMININ DOMAIN IV 2 (DOMAIN III B) .
 FT DOMAIN 1126 1158 LAMININ EGF-LIKE 5 (C-TERMINAL) .
 FT DOMAIN 1159 1208 LAMININ EGF-LIKE 6 .
 FT DOMAIN 1209 1265 LAMININ EGF-LIKE 7 .
 FT DOMAIN 1275 1324 LAMININ EGF-LIKE 8 .
 FT DOMAIN 1325 1334 LAMININ EGF-LIKE 9 (N-TERMINAL) .
 FT DOMAIN 1335 1529 LAMININ DOMAIN IV 3 (DOMAIN III C) .
 FT DOMAIN 1530 1562 LAMININ EGF-LIKE 9 (C-TERMINAL) .
 FT DOMAIN 1563 1612 LAMININ EGF-LIKE 10 .
 FT DOMAIN 1613 1670 LAMININ EGF-LIKE 11 .
 FT DOMAIN 1677 1771 IG-LIKE C2-TYPE DOMAIN 2 .
 FT DOMAIN 1772 1865 IG-LIKE C2-TYPE DOMAIN 3 .
 FT DOMAIN 1866 1954 IG-LIKE C2-TYPE DOMAIN 4 .
 FT DOMAIN 1955 2049 IG-LIKE C2-TYPE DOMAIN 5 .
 FT DOMAIN 2050 2148 IG-LIKE C2-TYPE DOMAIN 6 .
 FT DOMAIN 2149 2244 IG-LIKE C2-TYPE DOMAIN 7 .
 FT DOMAIN 2245 2343 IG-LIKE C2-TYPE DOMAIN 8 .
 FT DOMAIN 2344 2436 IG-LIKE C2-TYPE DOMAIN 9 .
 FT DOMAIN 2437 2532 IG-LIKE C2-TYPE DOMAIN 10 .
 FT DOMAIN 2533 2619 IG-LIKE C2-TYPE DOMAIN 11 .
 FT DOMAIN 2622 2720 IG-LIKE C2-TYPE DOMAIN 12 .
 FT DOMAIN 2721 2809 IG-LIKE C2-TYPE DOMAIN 13 .
 FT DOMAIN 2810 2895 IG-LIKE C2-TYPE DOMAIN 14 .
 FT DOMAIN 2896 2980 IG-LIKE C2-TYPE DOMAIN 15 .
 FT DOMAIN 2984 3162 EGFLIKE .
 FT DOMAIN 3163 3241 LAMININ G-LIKE 1 .
 FT DOMAIN 3245 3425 LAMININ G-LIKE 2 .
 FT DOMAIN 3518 3705 LAMININ G-LIKE 3 .
 SITE 65 67 HEPARAN SULFATE (POTENTIAL) .
 SITE 71 73 HEPARAN SULFATE (POTENTIAL) .
 SITE 76 78 HEPARAN SULFATE (POTENTIAL) .
 SITE 3615 3617 MEDiates MOTOR NEURON ATTACHMENT (POTENTIAL) .

FT DISULFID 199 212 BY SIMILARITY .
 FT DISULFID 206 225 BY SIMILARITY .
 FT DISULFID 219 234 BY SIMILARITY .
 FT DISULFID 285 297 BY SIMILARITY .
 FT DISULFID 292 310 BY SIMILARITY .
 FT DISULFID 304 319 BY SIMILARITY .
 FT DISULFID 325 337 BY SIMILARITY .
 FT DISULFID 332 350 BY SIMILARITY .
 FT DISULFID 344 359 BY SIMILARITY .
 FT DISULFID 368 381 BY SIMILARITY .
 FT DISULFID 375 394 BY SIMILARITY .
 FT DISULFID 388 403 BY SIMILARITY .
 FT DISULFID 428 479 BY SIMILARITY .
 FT DISULFID 764 773 BY SIMILARITY .
 FT DISULFID 766 780 BY SIMILARITY .
 FT DISULFID 783 792 BY SIMILARITY .
 FT DISULFID 795 811 BY SIMILARITY .
 FT DISULFID 814 829 BY SIMILARITY .
 FT DISULFID 816 839 BY SIMILARITY .
 FT DISULFID 842 851 BY SIMILARITY .
 FT DISULFID 854 869 BY SIMILARITY .
 FT DISULFID 871 889 BY SIMILARITY .
 FT DISULFID 891 910 BY SIMILARITY .
 FT DISULFID 911 930 BY SIMILARITY .
 FT DISULFID 927 947 BY SIMILARITY .
 FT DISULFID 947 966 BY SIMILARITY .
 FT DISULFID 967 985 BY SIMILARITY .
 FT DISULFID 985 1004 BY SIMILARITY .
 FT DISULFID 1005 1023 BY SIMILARITY .
 FT DISULFID 1023 1042 BY SIMILARITY .
 FT DISULFID 1042 1061 BY SIMILARITY .
 FT DISULFID 1061 1080 BY SIMILARITY .
 FT DISULFID 1080 1100 BY SIMILARITY .
 FT DISULFID 1100 1120 BY SIMILARITY .
 FT DISULFID 1120 1140 BY SIMILARITY .
 FT DISULFID 1140 1160 BY SIMILARITY .
 FT DISULFID 1160 1180 BY SIMILARITY .
 FT DISULFID 1180 1200 BY SIMILARITY .
 FT DISULFID 1200 1220 BY SIMILARITY .
 FT DISULFID 1220 1240 BY SIMILARITY .
 FT DISULFID 1240 1260 BY SIMILARITY .
 FT DISULFID 1260 1280 BY SIMILARITY .
 FT DISULFID 1280 1293 BY SIMILARITY .
 FT DISULFID 1293 1304 BY SIMILARITY .
 FT DISULFID 1304 1322 BY SIMILARITY .
 FT DISULFID 1322 1341 BY SIMILARITY .
 FT DISULFID 1341 1363 BY SIMILARITY .
 FT DISULFID 1363 1382 BY SIMILARITY .
 FT DISULFID 1382 1401 BY SIMILARITY .

RESULT 1.2

PVRL1_HUMAN	ID	PVR1_HUMAN	STANDARD;	PRT;	517 AA.
AC	Q15223;	Q75465;	Q9HB66;	Q9HBW2;	
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2002	(Rel. 41, Last annotation update)			
DE	Poivovirus receptor related protein 1 precursor (Herpes virus entry DE (Hvec) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR) CD11 antigen).				
GN	PVRL1 OR PRR1 OR HVEC.				
OS	Homo sapiens (Human).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	SEQUENCE FROM N.A. (ISOFORM DELTA).				
RN	MEDLINE=55237621; PubMed=772110;				
RA	Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C., Dubreuil P.				
RA	"cDNA characterization and chromosomal localization of a gene related to the poiovirus receptor gene.";				
RT	Gene 155:261-265 (1995).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM DELTA).				
RX	MEDLINE=98279152; PubMed=9616127;				
RA	Gerughty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J., Spear P.G.;				
RA	"Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor.";				
RL	Science 280:1618-1620(1998).				
RN	[3]				

SEQUENCE FROM N.A. (ISOFORM GAMMA).
 MEDLINE=21256041; PubMed=11356977;
 RX Lopez M., Cochchi F., Avitabile E., Leclerc A., Adelaide J., Campadelli-Fiume G., Dubreuil P.; "Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin (or pvr1-HIGR-Hvec) modulates positively and negatively susceptibility to hsv infection.";
 RT J. Virol. 75:5684-5691(2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
 MEDLINE=20392396; PubMed=10932188;
 RX Suzuki K., Hu D., Buscios T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.; "Mutations of PVR1L, encoding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal dysplasia"; Natl. Genet. 25:427-430 (2000).
 CC FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESSVIRUS (HSV-1, HSV-2 AND PSEUDOBACTERIUS VIRUS) ENTRY INTO CELLS.
 CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORMS ALPHA AND DELTA) AND SECRETED (ISOFORM GAMMA).
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA, DELTA (SHOWN HERE), AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- DISEASE: Defects in PVR1L are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPED1). It is responsible for allelic forms known as Margarita island form and Zlotogora-Ogur syndrome.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- DATABASE: NAME=PROW; NOTE=2.45-4.9 (2001);
 CC -!- WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
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 CC DR EMBL; X76400; CAA53980_2; ALT_INIT.
 CC DR EMBL; AF060231; AAC23798_1; .
 CC DR EMBL; AY029539; AAK33124_1; .
 CC DR EMBL; AF258867; AAC16648_1; JOINED.
 CC DR EMBL; AF196768; AAC16648_1; JOINED.
 CC DR EMBL; AF196769; AAC16648_1; JOINED.
 CC DR EMBL; AF196770; AAC16648_1; JOINED.
 CC DR EMBL; AF196771; AAC16648_1; JOINED.
 CC DR EMBL; AF196774; AAC16649_1; .
 CC DR EMBL; AF196788; AAC16649_1; JOINED.
 CC DR EMBL; AF196789; AAC16649_1; JOINED.
 CC DR EMBL; AF196790; AAC16649_1; JOINED.
 CC DR EMBL; AF196771; AAC16649_1; JOINED.
 CC DR EMBL; AF196772; AAC16649_1; JOINED.
 CC DR InterPro; IP0003006; 19_MHC.
 DR InterPro; IP003598; 19_C2.
 DR InterPro; IP003596; 19_v.
 DR Pfam; PF00047; ig_2.
 DR SMART; SM00449; Ig_3.
 DR SMART; SM00498; IgC2_2.
 DR SMART; SM00496; IgV_1.
 DR Call adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL. 30 POTENTIAL.

PT	CHAIN	31	517	POLIOVIRUS RECEPTOR RELATED PROTEIN 1.	
PT	DOMAIN	31	355	EXTRACELLULAR (POTENTIAL).	
PT	TRANSMEM	356	376	POTENTIAL.	
PT	DOMAIN	377	517	CYTOSLASMIC (POTENTIAL).	
PT	DOMAIN	44	131	IG-LIKE V-TYPE DOMAIN.	
PT	DOMAIN	165	233	IG-LIKE C2-TYPE DOMAIN 1.	
PT	DOMAIN	262	323	IG-LIKE C2-TYPE DOMAIN 2.	
PT	DOMAIN	437	444	POLY-GLY.	
PT	DOMAIN	445	449	POLY-GLY.	
PT	DISULFID	51	124	BY SIMILARITY.	
PT	DISULFID	172	226	BY SIMILARITY.	
PT	DISULFID	269	316	BY SIMILARITY.	
PT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	72	72	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	286	286	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	307	307	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).	
PT	VARSPLIC	335	352	EPPTPSPDPBHGRRAGPV -> AFCQLYPPGKGRTRAMF (IN ISOFORM GAMMA).	
PT	VARSPLIC	353	517	MISSING (IN ISOFORM GAMMA).	
PT	VARSPLIC	336	458	FPPTPSPDPHGRGRRAGPVPAIIGGVAGSSILLVLLIVVGIVV ALRERRHTPKDYSTKAGYPSKSYEEGKSYEEKEGGGERKVKUGGPH YPDSDSDDDEKKAQGPGUGGSSEEEGKSYEEKEGGGERKVKUGGPH -> KPRPQRQLGSAARLLAAGTVAFLVLLVAVTFFLNQRQ QKSPPETTDAGTDQPLSLOQPYDQYDGVSSSYHPSVRTRTEPRG PGRQQQKQEEDDLQKLSQLQPSRSSLVPEDIQVWHL ECP (IN ISOFORM ALPHA).	
PT	SEQUENCE	517	517	MISSING (IN ISOFORM ALPHA).	
SQ	VARSPLIC	459	517	AA; 5717 MW;	DF34CBAEC839EE60 CRC64;
Query Match Score 9.7%; Best Local Similarity 18.6%; Matches 67; Conservative Pred. No. 0.0014; Mismatches 50; Indels 158; Gaps 17;	Length 517;				
Qy	34	GETAYLPCCRFTLGPDQGPDIEMILSPADNOKVQDV	-----IIILYS-----GDK 78		
Db	44	GTDVVLHCSFA-----	-----NPLPSVKITQVTTWQKSTNGSKONVAINPSMVS 88	FT SIGNAL	1 31
Qy	79	IYDDYYQDLKGKRVHFTNSNDLKSGDASINVNLQSDIGTYQCKVKAQPVGNKKIQ--LT 136		FT CHAIN	32
Do	89	VLAPI----RERVEFLRPSFT--DGTLRLSRLEDEGYICEFATPEP-TGNRESQMLNT 141		FT PROPEP	? 348
Qy	137	VLLKPSGTROYDGGSEETI----GNDPKBSLPLIYEWKR-----	-----177	FT DOMAIN	47 119
Db	142	VMAKPTN--WIEGTQAVLERAKKGODDKVLUATCTSANGKPPSVSWTRLGKBEAYOBI 198		FT DOMAIN	147 204
Qy	178	-----LNSNQSLKP-----	-----TTLWAEMTSVPSVKN-----201	FT DOMAIN	232 298
Db	199	RNPNGTVTVISRYRLVPSREAHQSCLACIVNYHMDRFKESLTINQYEPETVLEGFDNW 258		FT DISULFID	54 112
Qy	202	-----ASTEV-----	-----SGTYSCTV 214	FT DISULFID	154 197
Db	259	YLQRMDVKLTCKADANPAPATEYHWTLLNGSLPKGVSEAQNRTLFFKGPNINYSLAGTYICEA 318		FT DISULFID	239 291
Qy	215	KNRVGSQDQLCQLRLDV-----BPSN--RAGTTAGLGLIITCC 260		FT CARBOHYD	67 67
Db	319	TNPJGTRSGQEVNITEPYTPSPHEHGRAGPVTAIGGVAGSSILLVLLIVVGIVVAL 378		FT CARBOHYD	149 149
Qy	261	R 261		FT CARBOHYD	269 269
Db	379	R 379		FT CARBOHYD	280 280
Qy	5	LCFVLLCGVADLTTRSLSLTTPEQMIKE--AKGETAYLPCCRFTLGPDQGPDIEMILSP 61		FT CARBOHYD	288 288
Db	15	LAAVLLSLSCPLAGQSVDPWAAVDMNLRKGDTAVLRCYL---EDGASKGAWLNRS 69		FT CARBOHYD	301 301
Qy	62	ADNQKVQDVILYSGDKIYDDYYQDLKGKRVHFTNSNDLKSGDASINVNLQSDIGTYQCK 121		FT CARBOHYD	37858 MW; 37858 MW;
Db	70	S-----IIFAGGDK-----WSVDRVST-----SCTR-----C-----146		FT CARBOHYD	37858 MW; 37858 MW;
Qy	122	VRCAPGVENKKTQIOTVLLRP-----SGTR-----C-----173		FT CARBOHYD	37858 MW; 37858 MW;
Db	114	VQRQHTPRTMQVLTQVQPPKIIDISNDMTINEGNTVLTCLATGKPEPAISWRHISPSA 173		FT CARBOHYD	37858 MW; 37858 MW;
Qy	147	-----YVD-----		FT CARBOHYD	37858 MW; 37858 MW;

Db	174 KPFENGQYLDIYGITRDQAGEYECSAENDVSFPDVKKVRRVVFAPTIQBEIKSGTVTGCR 233	:	FT DOMAIN 437	443	POLY-GLU.
					POLY-GLY. BY SIMILARITY.
Qy	157 DFLKCKCEPREGSLPLPYENOK---LSENQQLPLTLWAEITSPVTSVKNASTEYSGTSC 212	:	FT DISULFID 172	226	BY SIMILARITY.
					FT DISULFID 269 316 CARBOHYD 36 36 CARBOHYD 72 72 CARBOHYD 139 139 CARBOHYD 202 202 CARBOHYD 286 286 CARBOHYD 297 297 CARBOHYD 307 307 CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL). N-LINKED (GLCNAC. .) (POTENTIAL).
Db	234 SGLIRCE-GAGVPPPAFENYKGKEKLFGQ-Q-GIITIONFSRSLITVNTQBFGNYTC 291	:	FT DISULFID 51	124	BY SIMILARITY.
					FT DISULFID 269 316 CARBOHYD 36 36 CARBOHYD 72 72 CARBOHYD 139 139 CARBOHYD 202 202 CARBOHYD 286 286 CARBOHYD 297 297 CARBOHYD 307 307 CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL). N-LINKED (GLCNAC. .) (POTENTIAL).
Qy	213 TVKNRVGSDQCLLRDVLVPPSNRACTIAGAVIGVL---LALVIGLI 256	:	FT DISULFID 51	124	BY SIMILARITY.
					FT DISULFID 172 226 CARBOHYD 36 36 CARBOHYD 72 72 CARBOHYD 139 139 CARBOHYD 202 202 CARBOHYD 286 286 CARBOHYD 297 297 CARBOHYD 307 307 CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL). N-LINKED (GLCNAC. .) (POTENTIAL).
Db	292 VAANKLGTTNASPLIN--PFSTAQYGTGSACDLFSCMSLALTSSVI 337	:	FT DISULFID 51	124	BY SIMILARITY.
					FT DISULFID 51
RESULT 14					
PRY1_PIG	PRY1_PIG	STANDARD;	PRY1_PIG	515 AA;	57047 MW; BFA00320DDE3785 CRC64;
ID	PRY1_PIG		SEQUENCE	515	
AC	Q9GL76	PRY1_PIG	Query	9.5%	Score 129.5; DB 1; Length 515;
DT	16-OCT-2001 (Rel. 40, Created)		Match	9.5%	DB 1; Length 515;
DT	16-OCT-2001 (Rel. 40, Last sequence update)		Best Local Similarity	18.5%	DB 1; Length 515;
DT	15-JUN-2002 (Rel. 41, Last annotation update)		Matches	50	No. 0/0/23; Pred: 0.0/0.0/0.0; Gaps 18;
DE	Polyiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Nectin 1).		Indels	159	
DE	(PRY1_PIG) OR PRY1 OR HVEC.		Gaps	18	
OS	Sus scrofa (PIG)				
OS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OC	NCBI_TaxID=9823;				
OX	[1]				
RN	SEQUENCE FROM N.A.				
RP	Q9GL76; PubMed=11277703; Pubmed ID=11277703				
RX	RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;				
RA	"Porcine HvcC, a member of the highly conserved Hvc/nectin 1 family, is a functional alphaherpesvirus receptor." Virology 281:315-328 (2001).				
RC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPVESVIRUS (HSV-1, HSV-2 AND PSEUDOBORABLES VIRUS) ENTRY INTO CELLS.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.				
CC	-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.				
CC	-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.				
CC	-----				
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CC	-----				
CC	EMBL; AF308632; AAC30281.1; -.				
DR	HSSP; P05907; 1NEU.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003598; Ig_C2.				
DR	InterPro; IPR003600; Ig_Iglike.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_2.				
DR	SMART; SM00409; Ig_3.				
DR	SMART; SM00410; Ig_like_1.				
DR	SMART; SM00408; IgC_2.				
DR	SMART; SM00406; IgV_1.				
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.				
KW	POTENTIAL.				
FT	SIGNAL 1	30			
FT	CHAIN 31	515	POLIOVIRUS RECEPTOR RELATED PROTEIN 1.		
FT	DOMAIN 31	355	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 356	376	POTENTIAL.		
FT	DOMAIN 377	515	CYTOSMERIC (POTENTIAL).		
FT	DOMAIN 44	131	IG-LIKE V-TYPE DOMAIN.		
FT	DOMAIN 165	233	IG-LIKE C2-TYPE DOMAIN 1.		
FT	DOMAIN 262	323	IG-LIKE C2-TYPE DOMAIN 2.		
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=92112994; PubMed=1730768;				
RA	Kalilunki P., Trygavason K.;				
RA	"Human basement membrane heparan sulfate proteoglycan core protein: a 46-kDa protein containing multiple domains resembling elements of the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor." J. Cell Biol. 116:559-571 (1992).				
OC	Hom sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID=9606;					
RN	[1]				

RC	SEQUENCE OF 1018-1472 FROM N.A.	DR	InterPro; IPR000742; EGF 2.
RC	TISSUE=Colon;	DR	InterPro; IPR001438; EGF_II.
RX	MEDLINE=9136376; PubMed=1679479;	DR	InterPro; IPR003006; Ig_MHC.
RA	Murdock A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;	DR	InterPro; IPR003598; Ig_c2.
RT	"Primary structure of the human heparan sulfate proteoglycan from basement membrane (HSPG2/perlecan): A chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor.";	DR	InterPro; IPR002172; LDL_recept_A.
RT	"Heparan sulfate proteoglycan of human colon: Partial molecular cloning, cellular expression, and mapping of the gene (HSPG2) to the short arm of human chromosome 1.";	DR	InterPro; IPR00034; Laminin_B.
RT	Genomics 10:673-680(1991).	DR	InterPro; IPR002649; Laminin_EGF.
RJ	RP	DR	InterPro; IPR001791; Laminin_G.
RN	SEQUENCE OF 1018-1472 FROM N.A.	DR	InterPro; IPR000682; SEA_Domain.
RC	TISSUE=Fibrocarcoma;	DR	Pfam; PF00008; BCF; 4.
RX	MEDLINE=9136376; PubMed=1679479;	DR	Pfam; PF00047; Ig; 22.
RA	Dodge G.R., Kovalsky I., Chu M.L., Hassell J.R., McBride O.W., Yi H.F., Iozzo R.V.;	DR	Pfam; PF00052; laminin_B; 3.
RA	"Cloning of human heparan sulfate proteoglycan core protein, assignment of the gene (HSPG2) to 1p36.1--p35 and identification of a BamHI restriction fragment length polymorphism.";	DR	Pfam; PF00053; laminin_EGF; 7.
RT	Genomics 11:389-396(1991).	DR	Pfam; PF00054; laminin_G; 3.
RJ	RP	DR	Pfam; PF00057; ldl_recept_a; 4.
RN	SEQUENCE OF 1-21 FROM N.A.	DR	Pfam; PF001330; SPA; 1.
RC	TISSUE=Colon;	DR	PRINTS; PRO0010; EGFBLOOD.
RX	MEDLINE=9120860; PubMed=8168141;	DR	Prints; PD003031; Laminin_B; 3.
RA	Kallunki P., Eddy R.L., Byers M.G., Restila M., Shows T.B., Trygveason K.;	DR	SMART; SM00180; BGF_Lam; 6.
RA	"Cloning of human heparan sulfate proteoglycan core protein, assignment of the gene (HSPG2) to 1p36.1--p35 and identification of a BamHI restriction fragment length polymorphism.";	DR	SMART; SM00281; LamG; 3.
RT	Genomics 11:389-396(1991).	DR	PROSITE; PS00022; EGF_1; 9.
RJ	RP	DR	PROSITE; PS01186; EGF_2; 5.
RN	SEQUENCE OF 1-21 FROM N.A.	DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
RC	TISSUE=Fibrocarcoma;	DR	PROSITE; PS00025; LAM_G_DOMAIN; 3.
RX	MEDLINE=9120860; PubMed=8168141;	DR	PROSITE; PS01209; LDLR_A; 4.
RA	Kallunki P., Eddy R.L., Byers M.G., Restila M., Shows T.B., Trygveason K.;	DR	PROSITE; PS05068; LDLR_A; 2; 4.
RA	"Structural characterization of the complete human perlecan gene and its promoter.";	DR	PROSITE; PS00024; SEA; 1.
RT	Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;	FT	Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein; KW
CC	"Structural characterization of the complete human perlecan gene and its promoter.";	FT	Extracellular matrix; EGF-like domain; Immunoglobulin domain; Potential.
CC	-!- FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.	FT	CHAIN
CC	-!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers orstellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type IV.	FT	FT
CC	-!- SUBCELLULAR LOCATION: Extracellular.	FT	TG_LIKE_C2-TYPE DOMAIN 1.
CC	-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.	FT	LAMININ_EGF-LIKE_1_(N-TERMINAL).
CC	-!- CC AND O-LINKED OLIGOACCHARIDES.	FT	LAMININ_EGF-LIKE_1_(C-TERMINAL).
CC	-!- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.	FT	LAMININ_EGF-LIKE_2.
CC	-!- SIMILARITY: CONTAINS 10-5 LAMININ EGF-LIKE DOMAINS.	FT	LAMININ_EGF-LIKE_3.
CC	-!- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.	FT	LAMININ_EGF-LIKE_4_(INCOMPLETE).
CC	-!- SIMILARITY: CONTAINS 22 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.	FT	LAMININ_EGF-LIKE_5_(N-TERMINAL).
CC	-!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.	FT	LAMININ_EGF-LIKE_6.
CC	-!- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.	FT	LAMININ_EGF-LIKE_7.
CC	-!- SIMILARITY: CONTAINS 1 SEA DOMAIN.	FT	LAMININ_EGF-LIKE_8.
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CC	EMBL; X62515; CAA4373.1; -	FT	LAMININ_EGF-LIKE_9_(C-TERMINAL).
CC	EMBL; M05289; AAA2700.1; -	FT	LAMININ_EGF-LIKE_10.
CC	EMBL; M04283; AAA52699.1; -	FT	LAMININ_EGF-LIKE_11.
CC	EMBL; S76436; AAB1121.2; -	FT	LAMININ_EGF-LIKE_12.
CC	EMBL; I22078; -; NOT_ANNOTATED_CDS.	FT	LAMININ_EGF-LIKE_13.
CC	HSSP; P00740; 1EDM.	FT	LAMININ_EGF-LIKE_14.
CC	Siena; X2D PAGE; P9B10; -	FT	LAMININ_EGF-LIKE_15.
CC	GeneW; HGNC:3273; HSPG2.	FT	LAMININ_EGF-LIKE_16.
CC	MIM; 142461; -	FT	LAMININ_EGF-LIKE_17.
CC	InterPro; IPR005561; EGF-like.	FT	LAMININ_EGF-LIKE_18.

PT	DOMAIN	2829	2926	IG-LIKE C2-TYPE DOMAIN 14.
PT	DOMAIN	2927	3023	IG-LIKE C2-TYPE DOMAIN 15.
PT	DOMAIN	3024	3114	IG-LIKE C2-TYPE DOMAIN 16.
PT	DOMAIN	3115	3213	IG-LIKE C2-TYPE DOMAIN 17.
PT	DOMAIN	3224	3301	IG-LIKE C2-TYPE DOMAIN 18.
PT	DOMAIN	3301	3401	IG-LIKE C2-TYPE DOMAIN 19.
PT	DOMAIN	3402	3490	IG-LIKE C2-TYPE DOMAIN 20.
PT	DOMAIN	3491	3576	IG-LIKE C2-TYPE DOMAIN 21.
PT	DOMAIN	3577	3664	IG-LIKE C2-TYPE DOMAIN 22.
PT	DOMAIN	3665	3845	LAMININ G-LIKE 1.
PT	DOMAIN	3846	3883	EGF-LIKE 1.
PT	DOMAIN	3886	3924	EGF-LIKE 2.
PT	DOMAIN	3930	4105	LAMININ G-LIKE 2.
PT	DOMAIN	4106	4143	EGF-LIKE 3.
PT	DOMAIN	4145	4178	EGF-LIKE 4.
PT	DOMAIN	4203	4391	LAMININ G-LIKE 3.
PT	SITE	65	67	HEPARAN SULFATE (POTENTIAL).
PT	SITE	71	73	HEPARAN SULFATE (POTENTIAL).
PT	SITE	76	78	HEPARAN SULFATE (POTENTIAL).
PT	SITE	4151	4153	MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).
PT	SITE	4301	4303	MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).
PT	DISULFID	199	212	BY SIMILARITY.
PT	DISULFID	206	225	BY SIMILARITY.
PT	DISULFID	219	234	BY SIMILARITY.
PT	DISULFID	285	297	BY SIMILARITY.
PT	DISULFID	292	310	BY SIMILARITY.
PT	DISULFID	304	319	BY SIMILARITY.
PT	DISULFID	325	337	BY SIMILARITY.
PT	DISULFID	332	350	BY SIMILARITY.

Query Match 9.5%: Score 128.5; DB: 1; Length 4393;
 Best Local Similarity 23.3%; Pred. No. 0.04;
 Matches 50; Conservative 35; Mismatches 75; Indels 55; Gaps 11;

Qy	20	LSITTPQMIEKAGETAYLPCRFITLGPEQQLDIEWLLSPADNQKVQDVQVILYSGDKI	79
Db	3026	ISIDPSSITVO-QQDASPC--LHDGAAPSLEW-----	3058
Qy	80	YDDYYQDLKGRVHFTSNLKGDAISINVNLQLSDIGTYQCKVKRKAQGYGNKXIQL----	135
Db	3059	-KTRNOLEDNVHISPNS---GSITIVGTRPSNHGTYRCVASNAYGQAQSVVNLSTHG	3112
Qy	136	-TVLILPKSGTRCYDSEBIGNDFKLKC---EPKEGSLPLIYEWOKLHSNS-OKLPLTLW	188
Db	3113	PPTVSVLPPEGD-VWV---KVGAVTLECVSAGEPRSSA---RWTISSTPAKLEORT	3162
Qy	189	LAEMTS-PVISVKNSTEYSGTYSCTVKNRVGSDQ	222
Db	3163	YGLMDSHTRVLIQISSAKPSDAGTVCLANALGTAQ	3197

Search completed: July 9, 2003, 12:44:49
 Job time : 11 secs

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(c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:42:53 ; Search time 32 Seconds
(without alignments)

1680.572 Million cell updates/sec

Title: US-09-899-634C-2
Perfect score: 1359
Sequence: 1 MALLUCFVLLCGVADLTRLSL.....AVIGVILALVLIGIIFCCR 261

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaea:*

ALIGNMENTS

RESULT	1
Q9TU79	PRELIMINARY;
AC Q9TU79	PRT;
ID Q9TU79	319 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE Cossackie-adenovirus-receptor homolog (Fragment).	
GN CAR.	
OS Sus scrofa (Pig).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; NCFI_TaxID=9823;	
OX	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE-LIVER;	
RX MEDLINE-99422053; PubMed=10490761;	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	98.1	Q9TU79	Q9TU79	6	Q9TU79	Q9TU79 sus scrofa
2	92.7	93.5	Q8WWY3	6	Q8WWY3	Q8WWY3 bos taurus
3	1254	92.3	Q9TU80	6	Q9TU80	Q9TU80 canis familiaris
4	1238	91.1	Q9UKV4	4	Q9UKV4	Q9UKV4 homo sapiens
5	1223	90.7	344	11	Q9R067	Q9R067 ratmus norvegicus
6	1233	90.7	358	11	Q9R066	Q9R066 ratmus norvegicus
7	1216	89.5	352	11	Q9IW66	Q9IW66 mus musculus
8	1216	89.5	366	11	Q9DBJ8	Q9DBJ8 mus musculus
9	921	67.8	252	4	Q8WWY6	Q8WWY6 homo sapiens
10	676	49.7	200	4	Q8WWY7	Q8WWY7 homo sapiens
11	659.5	48.5	372	13	Q9OY50	Q9OY50 brachydanio
12	641	47.2	164	11	Q99KG0	Q99KG0 mus musculus
13	378.5	27.9	373	4	Q9H6B4	Q9H6B4 homo sapiens
14	366.5	27.0	373	11	Q8R373	Q8R373 mus musculus
15	362.5	26.7	373	11	Q92055	Q92055 mus musculus
16	338	24.9	89	4	Q8WWY8	Q8WWY8 homo sapiens

Query Match 98.7%; Score 1341; DB 6; Length 319;
Best Local Similarity 99.2%; Pred. No. 3.2e-112;
Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DR	EMBL; BC009371; AAH09371..1; -
DR	InterPro; IPR003599; Ig..
DR	InterPro; IPR003598; Ig_c2..
DR	InterPro; IPR003600; Ig_1-like..
DR	InterPro; IPR003006; Ig_MHC..
Pfam	PF00047; Ig..2.
DR	SMART; SM00409; Ig..2.
DR	SMART; SM00408; IgC2..2.
DR	SMART; SM00410; Ig_1-like..1.
KW	Hypothetical protein; Immunoglobulin domain.
SQ	SEQUENCE 373 AA: 41280 MW; FD215EB3B3C4335 CRC64;
Query Match	27.9%; Score 378..5; DB 4; Length 373;
Best Local Similarity	34.6%; Pred. No. 1..1e-25;
Matches	91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;
Qy	1 MALLCIVLICGVADITRSLSITTPQMIKEKAGETAYLPCRFILCPEDOGPLDIEWLLS 60
Db	1 MSLLLILL--VSYVGTGCTHTE --IKRVAEEKVTLPHHQQLPERDTLDIWLTT 54
Query Match	27.9%; Score 378..5; DB 4; Length 373;
Best Local Similarity	34.6%; Pred. No. 1..1e-25;
Matches	91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;
Qy	1 KVKKAPGVGNKKIQLTLLKPSGTGGTTRYVDSSEIGNDFKLKCEPKEGSPLPYEWKL-- 178
Db	55 --DNBEGNOKVITYSSRHVNNLTEEQGRVAFASNFL-AGDASLQIEPLKPSDEBRYTC 111
Query Match	27.9%; Score 378..5; DB 4; Length 373;
Best Local Similarity	34.6%; Pred. No. 1..1e-25;
Matches	91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;
Qy	121 KVKKAPGVGNKKIQLTLLKPSGTGGTTRYVDSSEIGNDFKLKCEPKEGSPLPYEWKL-- 178
Db	112 KVKNNSGRYVSHVILKVLVRPSKPKECLEGTELSDTLQCESSSGTPIVYYWQIRE 171
Query Match	27.9%; Score 378..5; DB 4; Length 373;
Best Local Similarity	34.6%; Pred. No. 1..1e-25;
Matches	91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;
Qy	179 --SNSQKRLPTLWLAENTSP-VTISVKAJSTESTGTSCTVNRVGSQOCLLRDWPSPSNR 235
Db	231 IGMVAGAVTGIVLLALVIGHLIF 253
RESULT 14	
Q8R373	PRELIMINARY; PRT; 373 AA.
ID	Q8R373; AC
RA	Q8R373; Q8R373; AC
DT	01-JUN-2002 (TREMBLrel. 21, Created)
DR	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
SQ	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB	RIKEN cDNA 9030425E11 gene.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
OX	NCBI_Taxid=10090;
RN	[1] --
RP	SEQUENCE FROM N.A.
RA	Strausberg R.;
DT	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC026447; AAH26447..1; 5
SQ	SEQUENCE 373 AA: 41214 MW; 9C668848AF95512 CRC64;
Query Match	27.0%; Score 366..5; DB 11; Length 373;
Best Local Similarity	35.3%; Pred. No. 1..3e-24;
Matches	83; Conservative 48; Mismatches 95; Indels 9; Gaps 5;
Qy	29 IEKAKGTTAYLPCRFILCPEDOGPLDIEWLLSPADNQKVDFQVILSGDKTYDDYODLK 88
Db	22 IKRVAEEKVTLPHHQQLPEKDITLWLT..-DNEGNGQKVITYSSRHVNNLTEEQK 79
Query Match	27.0%; Score 366..5; DB 11; Length 373;
Best Local Similarity	35.3%; Pred. No. 1..3e-24;
Matches	83; Conservative 48; Mismatches 95; Indels 9; Gaps 5;
Qy	89 GRVHFSTSNDLKSGDASINVNLQSLDIGTYOCKVKAPGVENKKIQLTLLKPSGTRCYV 148
Db	80 GRVAFASNFL-AGDASLQIEPLKPSDEBRYTCVNSHVLKVLVRPSKPCKEL 138
Query Match	27.0%; Score 366..5; DB 11; Length 373;
Best Local Similarity	35.3%; Pred. No. 1..3e-24;
Matches	83; Conservative 48; Mismatches 95; Indels 9; Gaps 5;
Qy	149 DGSEEGNDFKLKCEPKEGSPLPYEWKL---SNSQKRLPTLWLAEMTSP-VISVKNAS 203
Db	139 EGEPTESSDLTQCEASGTKPIVYQRIREKEGEDDEHLPKPSRDIYNNPGRVLQNLT 198
RESULT 13	
Q9H6B4	PRELIMINARY; PRT; 373 AA.
ID	Q9H6B4; DT
RA	Q9H6B4; SEQUENCE FROM N.A.
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DR	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DS	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	CDNA: FLJ22415 Fis, clone HR08561 (Hypothetical 41.3 kDa protein)
DC	Homo sapiens (Human)
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
OX	[1] --
RP	SEQUENCE FROM N.A.
RA	Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; NEDO human cDNA sequencing project.; Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DT	[2] SEQUENCE FROM N.A.
DS	TISSUE-MUSCLE;
DE	Strausberg R.;
OC	Submittet (JUN-2001) to the EMBL/GenBank/DBJ databases.
OX	EMBL; AK026068; BAB15347..1;
RP	[3] --
RA	204 TBYSGGYSCTVKNRVSQDOCLRLDVPPSNRAGTAGIVGVLLAVLGLLIF 258

Db 199 MASSLYQCTAGNEAGKESCVVRV-TVQYQSIGMAGAVTGVAGAALIFLLIW 252

RESULT 15

Q92055	PRELIMINARY;	PRT;	373 AA.
AC	Q92055;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-MAR-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Adipocyte-specific protein 5.		
GN	ASPs.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX			
RN	[1] TAXID=10090;		
RN	SEQUENCE FROM N.A.		
RA	Tsuruga H.;		
RT	"Adipocyte-specific protein 5, a novel protein upregulated during adipocyte differentiation."		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB040490; BAB68503.1;		
DR	InterPro; IPR003006; IG_MHC.		
DR	Pfam; PF00047; ig_2.		
SQ	SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;		

Query Match 26.7%; Score 362.5; DB 11; Length 373;
 Best Local Similarity 34.9%; Pred. No. 3.1e-24;
 Matches 82; Conservative 48; Mismatches 96; Indels 9; Gaps 5;

QY 29 IEKAKGETAYLPCKRPTLGPBDQGFLDIEWILSPADNQKVDFQVILYSGDKITYDDYYQQLK 88

Db 22 IKRYAAEKVTLPCPHOLGLPEKDTLDIEWILT--DNEGNGQKVITYSSRHVVNLTEBOK 79

QY 89 GRVHFTSNDLKGDSASINVNQLSDIGITVQCKVKAPEGVNGKKIQLTVLLKPSGTRCYV 148

Db 80 GRVAFASNFL-AGDASLQEPLKSDEGRYTCRVKNSGRYVWASHVILKALVRSKPKBL 138

QY 149 DGSEBEEIGNDFKLKCEPKEGSLPLLYEWQKLU---SNSQKLPTLWAEMTSP-VISVKMAS 203

Db 139 EGEPPTEGSDLTLCQESASCTKPIVYWWIREKEGEDDEHLPKSKRIDNNPGRVLLQNLIT 198

QY 204 TEYSGTYSCTVQNRVGSDQCLLRDVPVPSNRAGTIAGAVIGVILLALYLIGLIF 258

Db 199 MASSLYQCTAGNEAGKESCVVRV-TVQYQSIGMAGAVTGVAGAALIFLLIW 252

Search completed: July 9, 2003, 12:45:29
 Job time : 34 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 11:13:22 ; Search time 1878 Seconds
 (without alignments)
 4044.639 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLICFVILCGVADLIRSL.....AVIGVLLALVLGLIIFCCR 261

Scoring table: BLOSUM62

xgapop 10.0 , xgapext 0.5
 xgapop 10.0 , xgapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
 -MODEL=frame_p2n.model -DEV=x1h
 -Q=/GenBank -QFORMAT=fasta -DB=GenBank -DBFORMAT=FASTA -SUFFIX=ige -MINMATCH=0.1 -LOOPLEN=0 -LOOPEXT=0
 -UNIT=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
 -DOCIGN=200 -THR_SCORE=90 -THR_MAX=100 -MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFORMAT=PTC -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US-0999634 @CGN 1 1 1687 @runat 09/07/2003 11:13:38 16343 -NCPU=6 -ICPU=3
 -NO_MMAPP -LARGEQUERY -SCORES=0 -WAIT -DSPBTCK=100 -LONGLOG
 -DEV TIMEOUT=1200 -WARN TIMEOUT=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=0.7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7

Result No.	Score	Query Match Length	DB ID	Description
1	1341	98.7	959 4	AF109646 AF109646 Sus scrofa
2	1270	93.5	1184 4	AY033651 Bos tauru
3	1254	92.3	959 4	AF109645 Canis familiaris
4	1238	91.1	1033 9	AF124598 Homo sapiens
5	1238	91.1	2354 9	HSU090716 U90716 Human cell line
6	1238	91.1	2434 6	AR157886 AR157886 Human sequence
7	1238	91.1	2434 9	Y07593 H. Sequence
8	1238	91.1	2447 9	BC010536 BC010536 Homo sapiens
9	1238	91.1	2537 9	BC003684 BC003684 Homo sapiens
10	1238	91.1	3060 6	AX089948 AX089948 Sequence
11	1238	91.1	3060 6	AX338962 AX338962 Sequence
12	1238	91.1	3060 6	AX338962 AX338962 Sequence
13	1238	91.1	3060 6	AX362455 AX362455 Sequence
14	1238	91.1	3060 6	AX403617 AX403617 Sequence
15	1238	91.1	3060 6	AX454634 AX454634 Sequence
16	1238	91.1	3060 6	AK91172 Sequence
17	1238	91.1	3276 6	AX098210 AX098210 Sequence
18	1233	90.7	1033 10	AF109643 AF109643 Rattus norvegicus
19	1233	90.7	1076 10	AF109644 AF109644 Rattus norvegicus
20	1224	90.1	1095 6	ARI44703 ARI44703 Sequence
21	1224	90.1	1584 6	ARI44702 ARI44702 Sequence
22	1216	89.5	1098 10	MMU09175 MMU09175 Mus musculus
23	1216	89.5	1206 10	MMU09175 MMU09175 Mus musculus
24	1216	89.5	1515 6	ARI44704 ARI44704 Sequence
25	1216	89.5	1669 10	MMU09175 MMU09175 Mus musculus
26	1216	89.5	1696 10	BC016457 BC016457 Mus musculus
27	1145	84.3	17058 2	AC012414 Homo sapiens
28	1133	83.4	1522 9	HN803355 ALB834140 Homo sapiens
c	29	1133	83.4	108122 2 AC116905 Homo sapiens
30	1131	83.2	167605 2 AC068446 Homo sapiens	
31	1131	83.2	174104 2 AC060814 Homo sapiens	
32	1103.5	81.2	152318 2 ALJ62851 Homo sapiens	
33	1103.5	81.2	166239 9 HS214G4 Homo sapiens	
34	1103.5	81.2	340009 HS214G4 Homo sapiens	
35	921	67.8	759 9 AY072912 Homo sapiens	
36	875	64.4	64976 2 AC026256 Homo sapiens	
37	676	49.7	9 AY072931 Homo sapiens	
38	659.5	48.5	1883 5 AF268197 Danio rerio	
39	641	47.2	1312 10 BC004680 Mus musculus	
40	407	29.9	1296 9 AB079879 Homo sapiens	
41	402.5	29.6	1905 9 BC034411 Homo sapiens	
42	29.5	1287 10 AB079880 Mus musculus		
43	378.5	27.9	2307 9 BC009371 Homo sapiens	
44	378.5	27.9	2458 6 AX358976 Sequence	
45	378.5	27.9	2458 6 AX362369 Sequence	

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database : GenBank

1: gb_ba: *
 2: gb_btg: *
 3: gb_in: *
 4: gb_om: *
 5: gb_ov: *
 6: gb_pat: *
 7: gb_ph: *
 8: gb_pl: *
 9: gb_pr: *
 10: gb_ro: *
 11: gb_sts: *
 12: gb_sy: *
 13: gb_un: *
 14: gb_vn: *
 15: em_ba: *
 16: em_fun: *
 17: em_hun: *
 18: em_in: *
 19: em_mai: *
 20: em_on: *
 21: em_or: *
 22: em_ov: *
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 24: em_ph: *
 25: em_pl: *
 26: em_ro: *
 27: em_sb: *
 28:

ALIGNMENTS

AF109646 AF109646 959 bp mRNA linear MAM 06-OCT-1999
 LOCUS Sub scrofa coxsackie-adenovirus-receptor homolog (CAR) mRNA,
 DEFINITION partial cds.
 ACCESSION AF109646
 VERSION AF109646.1 GI:6013138
 KEYWORDS SOURCE Sus scrofa.
 ORGANISM Sus scrofa.
 REFERENCE 1. (bases 1 to 959)
 AUTHORS Fechner, H., Haack, A., Wang, H., Wang, X., Eizema, K., Pauchinger, M., Schöemaker, R., Veghei, R., Houtsmaier, A., Schultheiss, H.P., Lamers, J. and Poller, W.
 TITLE Expression of coxsackie adenovirus receptor and alphav-integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers
 JOURNAL Gene Ther. 6 (9), 1520-1535 (1999)
 MEDLINE 99422053
 PUBMED 10490761
 REFERENCE 2. (bases 1 to 959)
 AUTHORS Fechner, H., Haack, A., Wang, H., Wang, X., Wiese, A., Lamers, J.M.J. and Poller, W.
 TITLE Direct Submission
 JOURNAL Submitted (25-NOV-1998) Department of Cardiology and Pneumology, Benjamin Franklin University Hospital, Hindenburgdamm 30, Berlin 12200, Germany
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 ASINVNLQLSINGTYCKVKRGPKGVANKKOTIVLKGKPSGRCYDGESETINDKL
 KCPKEKSPLIYEWQKLSNSQDQPTWLAEMSPVSKRNATERSGTYCTVKRV
 GSDQCLRLDVDPVPSNAGTAGAAGVGLVLAALIGLIVFCCHKKREKEYKEVHD
 IREDVPPPKSRTSTARSLVGLNSHSLSMSPSMNEGISKIQIN"
 BASE COUNT 290 a 200 c 219 g 250 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.14e-123 Length: 959
 Score: 1341.00 Matches: 258
 Percent Similarity: 99.62% Conservative: 1
 Best Local Similarity: 99.23% Mismatches: 1
 Query Match: 98.68% Indels: 0
 DB: Gaps: 0
 US-09-899-634C-2 (1-261) x AF109646 (1-959)

RESULT 2 AF033651
 LOCUS AF033651
 DEFINITION Bos taurus coxsackie virus and adenovirus receptor BCAR mRNA, complete cds.
 ACCESSION AF033651
 VERSION AF033651.1 GI:18175273
 KEYWORDS SOURCE Bos taurus.
 ORGANISM Bos taurus.
 REFERENCE 1. (bases 1 to 1184)
 AUTHORS Thoelen, I., Keyaerts, E., Lindberg, M. and Van Ranst, M.
 TITLE Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor. Biophys. Res. Commun. 288 (4), 805-808 (2001)
 JOURNAL Biophys. Res. Commun.
 MEDLINE 21547769
 PUBMED 1168979
 REFERENCE 2. (bases 1 to 1184)
 AUTHORS Thoelen, I., Keyaerts, E., Lindberg, A.M. and Van Ranst, M.
 TITLE Direct Submission
 JOURNAL Submitted (03-APR-2001) Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven B-3000, Belgium
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 61 ProkalaAspAsnGlnLysValAspGlnValLeuLeuTyrSerGlyAspLysLeuTyr 80

ORIGIN

Alignment Scores:	1.95e-112	VERSION	Y07933.1
Pred. No.:	1238.00	KEYWORDS	G1;881446 kappa receptor protein; coxsackie and adenovirus receptor protein.
Score:	94.25%	SOURCE	GI:881446
Percent Similarity:	94.27%	ORGANISM	Homo sapiens.
Best Local Similarity:	89.27%	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Query Match:	91.10%	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		REFERENCE	1 (bases 1 to 2343)
		REFERENCES	Bernelson J M, Cuningham T A, Dromerick G, Kurt-Jones P A

QY	81	ASDASPTYTYrgInAspIleuIysGlyArgValHisPheThrSerAsnAspIleuIysSer	100
Db	300	GATGACTACTTCCAGCTCTGAAAGGCCGATTCATTTACGATAATGATCCTAACCT	359
QY	101	GLYAspAlaSerIleasnValThrAspLeuGlnLeuSerAspIleuIysGlyThrTyrgInCys	120
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		/clone_id="NTH MGC_12"	
		/lab_host="DH10B"	
		/note="Vector: pCMV-SPORT6"	
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Db	420	AAGTGAaaaAGCTCCGGTGTGCAATAAGAGATTCCTGGTAGTCTGGTAGTCTGGTAG	479
QY	161	LysCysGluProIysGluGlyArgLeuIysSerLeuProLeuLeuIysGlyArgAspPhenylsLeu	180
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Db	181	SerGlyIysLeuProThrLeuItpLeuLalaGluMetThrLeuProValIysSerValIys	200
Db	600	TCAAGAAAATGGCCACTCTCATGTTAGCGAAATGACTTCCTCTGTATATCTGAAA	659
QY	201	AstraLasThrGlyArgTyrySerGlyThrIysSerCysThrValIysAsnArgValGlySer	220
Db	660	AATGCCCTCTCTGAGTACTCTGGACATACAGCTGAGCTGAGTGTGAGCTGAGTGTGCTCT	719
QY	221	AspGlnCysLeuIleuArgLeuIysValProProSerAspArgAlaGlyThrIleAla	240
Db	720	GATCAGTGCTGTTGCGCTAACAGTTCCTCAATAAAGCTGACTAATGCA	779
		BASE COUNT	742
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		Alignment Scores:	
		Pred. No.: 1.97e-112	Length: 2447
		Score: 1238.00	Matches: 233
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		Query Match: 91.10%	Indels: 0
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Db	76	ATGGCCGCTCCCTGCTCTGCTGCTCTGCTGGAGTAGCTGCAAGAGTTG	135
QY	21	SerIleThrProGlyGlnMetIleGlyIysAlaIysGlyLhrAlaIysLeuPro	40
Db	136	ACTATCTCTCTGAGAGATGATGAGCTGAAAGCCAAAGGGAACATGCCATCTGCCG	195
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		REFERENCE	BC010536
		DEFINITION	2447 bp mRNA linear
		LOCUS	BC010536
		DEFINITION	Human papillomavirus receptor, clone
		ACCESSION	MG:17118 IMAGE:3456544, mRNA, complete cds.
		VERSION	BC010536
		KEYWORDS	BC010536.1 GI:14714774
		SOURCE	MGC.
		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		REFERENCE	1 (bases 1 to 2447)
		AUTHORS	Straussberg,R.
		TITLE	Direct Submission
		JOURNAL	Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		REMARK	NIH-MGC project URL: http://mgc.ncbi.nih.gov
		COMMENT	Contact: MGC help desk Email: cgaps-r@mail.nih.gov
		Tissue Procurement:	AIACC
		CDNA Library Preparation:	Life Technologies, Inc.
		CDNA Library Arrayed By:	The I.M.A.G.E. Consortium (IIML)
		DNA Sequencing by:	Baylor College of Medicine Human Genome Sequencing Center
		Sequencing Center:	BCM-HGSC
		Center code:	
		Web site:	http://www.hgsc.bcm.tmc.edu/cdna/
		Contact:	villalon@bcm.tmc.edu
		Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Teiford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.	

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium at: <http://image.lnl.gov>
 Series: IRAK Plate: 19 Row: f Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503172.
 Location/Qualifiers

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 /tissue_type="Cervix, carcinoma"
 /clone_id="NTH MGC_12"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

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Db 822 GGACCATATTAGGAACCTTGCTGCTATGGCTCATGCTTATCATTGTTGTG 881
 Qy 261 Arg 261
 Db 882 CGT 884

RESULT 10
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 LOCUS Sequence 106 from Patent WO0073452.
 DEFINITION
 ACCESSION AX055476
 VERSION AX055476.1 GI:12228735
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3060)
 AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tumas, D., Watancabe, C.K. and Wood, W.I.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Genentech, Inc. (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 1094 a 559 c 569 g 837 t 1 others
 ORIGIN 1. 3060
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 Score: 1238.00 Matches: 233
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 Best Local Similarity: 89.27% Mismatches: 15
 Query Match: 91.10% Indels: 0
 DB: Gaps: 0

US-09-899-634C-2 (1-261) x AX055476 (1-3060)

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 Db 77 ATGGCGCTCCGCTGCTGCTGCTCTGCTGGAGTAGGATTTCGCCAGAGTTG 136
 Qy 21 SerIleThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyroLeuPro 40
 Db 137 AGTATCACTCTCTGAAGAAGATGATTCGAAGAAACTGCCTATCTGCCA 196
 Qy 41 CySArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluIlePheLeuSer 60
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 Qy 81 AspAspThrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuSer 100
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 Qy 101 GlyAspAlaSerIleAsnValThrAsnLeuSerAspIleGlyThrThrGlyAspIleTyr 120
 Db 377 GGAGATGCTCATATAATGTAACGAAATTACACTGTCAGATATGGCACATACAGTC 436
 Qy 121 LysValAspLysAlaProDlyValGlyAsnLysLysIleGluLeuThrValLeuLeuLys 140
 Db 437 AsnGtGAAAAGCTCCCTGGTGTGCAATTAAGAGATTCATCTGGTAGTCTGTGTAAG 496
 Qy 141 ProSerGlyThrArgCysTyrValAspLysSerGluGluIleLysAspPheAspLeu 160
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RESULT 11
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 LOCUS Sequence 9 from Patent WO016319.
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 ACCESSION AX089948
 VERSION 1 GI:13443985
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3050)
 AUTHORS Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Tumas, D., Watancabe, C.K. and Wood, W.I.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Genentech, Inc. (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 1094 a 559 c 569 g 837 t 1 others
 ORIGIN 1. 3060
 /db_xref="taxon:9606"
 Alignment Scores:
 Pred. No.: 2.61e-112 Length: 3060
 Score: 1238.00 Matches: 233
 Percent Similarity: 94.25% Conservative: 13
 Best Local Similarity: 89.27% Mismatches: 15
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US-09-899-634C-2 (1-261) x AX089948 (1-3060)

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 Qy 21 SerIleThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyroLeuPro 40
 Db 137 AGTATCACTCTCTGAAGAAGATGATTCGAAGAAACTGCCTATCTGCCA 196
 Qy 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspIleLeuThrArgSerIeu 20
 Db 77 ATGGCGCTCCGCTGCTGCTGCTGCTGCTGGAGTAGGATTTCGCCAGAGTTG 136
 Qy 21 SerIleThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyroLeuPro 40
 Db 137 AGTATCACTCTCTGAAGAAGAACTGCCTATCTGCCA 196
 Qy 41 CySArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluIlePheLeuSer 60
 Db 197 TCGAACATTTCAGCTCCGAGACAGGAGCCGCTGGACATCGAGTGTGATATCA 256
 Qy 61 ProAlaAspAsnGlnLysValAspGlnValIleLeuThrSerGlyAspLysIleTyr 80

Best Local Similarity: 89.27% Mismatches: 0
 Query Match: 91.10% Index: 0
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US-09-899-634C-2 (1-261) x AX358962 (1-3060)

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 317 GATGACTACTCCAGTCGAAGGCCGAGTACATTACGAGTAATGCTCAATCT 376
 101 GLYASPALSERLAsnValThrAlaLeuGlnLeuSerAspIleGlyThrValCys 120
 377 GGTGTGCACTAATGPAACGATTACAACGTCAGATATGGCACATAAGTGC 436
 121 LysValLysValAspProGlyValGlyAspLysValSerIleGlnLeuLys 140
 437 RAGCTGAAAGCTCTGGTGTGAAATAGAGATCTGAGATCTGAGTCTTGTAAG 496
 161 LysCysGluProLygIleGlySerLeuProLeuAlaGluMetThrSerProValleuLys 200
 557 AAATGTAACCAAAAGAGGCTTCAATTACAGTATGTCGAAATGTCGCA 180
 181 SerGlnIleLeuProThrLeuIleGluAlaGluMetThrSerProValleuLys 200
 617 TCACAGAAAATGCCACTCTAGGTTAGCAGAAATAGACTCATCTGTTAA 676
 201 AsnAlaSerThrGlyIleGlySerCysThrAlaLysAsnArgValGlySer 220
 677 AATGCCTCTCTGAGTACTCGGGACATACGCTTACACTCAGAACAGTGTGCT 736
 221 AspGlnCysIleLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
 737 GATCAGTGCCTGCTGGCTAAACGTTGCTCTCAATAAAGTGTGACTATTGCA 796
 241 GlyAlaValIleGlyValLeuLeuLeuValLeuLeuIleLeuIlePhcysCys 260
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 261 Arg 261
 Db Qy 857 CGT 859

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 VERSION AX358962.1 GI:16675382
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.

REFERENCE 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I., Secreted and transmembrane polypeptides and nucleic acids encoding the same patent: WO 0193983-A 215 13-DEC-2001; Genentech Inc. (US) Location/Qualifiers 1. .3060 /organism="Homo sapiens" /db_xref="taxon: 9006"
 BASE COUNT 1094 a -559 c 569 g 837 t 1 others
 ORIGIN

FEATURES source
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 LOCUS DEFINITION Sequence 215 from Patent WO0208288.
 ACCESSION AX362455
 VERSION AX362455.1 GI:18694685
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.

Alignment Scores:
 Pred. No.: 2.618-112 Length: 3060
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 Percent Similarity: 94.25% Conservative: 13

GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.

SUMMARIES

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(without alignments)
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Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blastm62 -TRANS=human40.cdi
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3	1238	91.1	2434	2.4	ABL6022 Human coxsackie-ad
4	1238	91.1	2940	2.4	ABL8821 Human angiogenes
5	1238	91.1	3059	2.4	PROT723 CDNA Human PROT723 CDNA
6	1238	91.1	3060	2.2	AAFA224 Human PROT723 nucl
7	1238	91.1	3060	2.2	AAFA4263 Human PROT723 cDNA
8	1238	91.1	3060	2.4	ABK3643 CDNA encoding huma
9	1238	91.1	3276	2.2	AAF98715 Human late stage o
10	1238	91.1	3963	2.3	ABV25220 Human prostate exp
11	1238	91.1	1584	1.9	AAV28445 Human coxsackievir
12	1224	90.1	1584	1.9	AAV28446 Mouse coxsackievir
13	1216	89.5	1128	1.9	ABA05811 Mouse coxsackievir
14	1216	89.5	1301	1.9	ABV50439 Adenovirus PACS2
15	1142	84.0	834	2.0	AAV72025 Adenovirus SCAR.RG
16	1142	84.0	1194	2.0	AAV72027 Adenovirus PACSG2S
17	1142	84.0	1194	2.0	AAH76081 Rat coxsackie-adeno
18	800	58.9	578	2.2	AAH76081 Human cDNA SEQ ID
19	407	29.9	1758	2.2	ABK35611 Human immunoglobul
20	407	29.9	1853	2.2	ABK35626 Human ovarian anti
21	395	29.1	762	2.4	ABQ54549 Human A236 variant
22	379.5	27.9	1948	2.2	AAAC84114 Human A236 polypep
23	378.5	27.9	1122	2.2	AAAC84115 Human A236 variant
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27	378.5	27.9	2458	2.0	AA23341 Human PROT63 nucle
28	378.5	27.9	2458	2.1	AACT87173 Human PROT63 prote
29	378.5	27.9	2458	2.2	AAZ24377 Human PROT63 nucle
30	378.5	27.9	2458	2.2	AAZ44262 Human PROT63 nucle
31	378.5	27.9	2458	2.2	ABL95592 Human angiogenesis
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40	362.5	26.7	1927	2.2	AAH76756 Human cDNA SEQ ID
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42	357	26.3	811	2.2	AAH76756 Human A33 antigen.
43	351.5	25.9	2565	1.8	AAH76269 Human intestine ce
44	351.5	25.9	2793	2.2	AAH76269 Human A33 coding s
45	351.5	25.9	2793	2.2	AAH76269 Human A33 coding s

ALIGNMENTS

RESULT 1
ID AAV50429
XX AAV50429 standard; cDNA; 2354 BP.
AC AAV50429;
XX DT 07-DEC-1998 (first entry)
XX Human coxsackievirus and Ad2 and Ad5 receptor (HCAR) cDNA.
XX HCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
XX Ad5 receptor; human; infection; vaccine; gene therapy; ds.
XX Homo sapiens.
XX Key
PH FT
PT CDS
Key
Location/Qualifiers
1.1098
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PN WO9833819-A1.
XX
PD 06-AUG-1998.
XX
PR 30-JAN-1998; 98WO-US01724.
XX
PA (UNIV) UNIV NEW YORK STATE.
XX
PI Philipson L, Tomko RP;
XX
DR WPI; 1998-437397/37.
DR P-PSDB; AAW69697.
XX
PT DNA encoding human receptor for adenovirus C and coxsackievirus B -
susceptible to transformation by adenoviral vectors in gene therapy
PT
XX
PS Claim 2; Page 64-67; 88pp; English.
CC This cDNA molecule codes for human HCAR protein (see AAW69697) that
CC serves as a cellular receptor for adenoviruses of the serotypes 2
CC and 5 (subgroup C) and for the group B coxsackieviruses. It was
CC obtained by screening newborn human esophagus and pancreas islet
CC cell cDNA libraries using mouse MCAR clone RTMCAR-4 (see AAV5430)
CC as probe. The invention also provides host cells transformed with
CC DNA molecules encoding HCAR or MCAR and methods of producing the
CC recombinant proteins or their derivatives. These proteins,
CC their extracellular domains, as well as oligopeptides (see
CC AAW69699-708) which bind viruses, are also provided. Isolated HCAR or
CC MCAR proteins or their fragments or variants are used to prevent
CC or treat virus infections. Expressing the DNA in cells which lack
CC these viral receptors renders the cells susceptible to
CC transformation by adenoviral vectors carrying genes for gene
CC therapy.
XX
SQ Sequence 2354 BP; 710 A; 417 C; 470 G; 757 T; 0 other;

Alignment Scores:
Pred. No.: 5.69e-123 Length: 2354
Score: 1238.00 Matches: 233
Percent Similarity: 94.25% Conservative: 13
Best Local Similarity: 89.27% Mismatches: 15
Query Match: 91.10% Indels: 0
DB: 19 Gaps: 0

US-09-899-634C-2 (1-261) x AAV5429 (1-2354)

QY 1 MetalalauLeuLeuCysPheValleuLeuCysGlyValalaaspLeuThrArgSerieu 20
1 ATGCCGTCCTGGCGTGTGCTGCTCCCTGGAGATTTCCCAAGAGTTTG 60
QY 21 SerilethrhrProgluLysMetIleGluLysAlaLysGlyGluThrAlaLysLeuro 40
61 AGTATCACTCTCTGAAGGATGATGATGATGAAAGCCAAAGGGAAACTCTACCTCTGCCTA 120
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluLysLeuro 60
121 TGCAAATTTCAGCTTAGTCGGAGAACAGGGACCGCTGGACATTCGAGTCGCTGATATCA 180
61 ProAlaAspGlnGlyLysValaSpGlnVallelleLeuYrsSerGlyAspLysLeuYrs 80
181 CCAGCTGATCATCAGAAAGGGGGATCAAGGATTTATTCATCTGGAGACAATAT 240
QY 81 AspAspPtyrTyrGlnAspIleAspIleAspIleAspIleAspIleAspIleAspIleAsp 100
241 GATGACTACTATCCAGATCTGAAGGCCGCGTACATTACAGATACTGATGCTGATGCTAATCT 300
QY 101 GlyspalAspSerIleAsnValThrAsnLeuGlnIleSerAspIleGlyThrTyrGlnGly 120
,Db 301 GGTGATGCACTCAATAATGTAAACGGATTACAATGTCAGATATTGGCACCATATCAGTGC 360

QY 121 LysValIlysLysalaProGlyValGlyAsnLysLysIleGlnLeuThrValleuLys 140
Db 361 AAAGTGAGAAAAGCTCTGGTGTGCAATAAGAAGATTCATCTGGTACTGCTGTAAG 420
QY 141 ProSerGlyThrArgCysTyrValAspGlySerGluLysIleGlyAsnAspPhelySleu 160
Db 421 CCTTCAGSTGGGAGATGTTACGGTGTAGATCTGAAGAAATGGAGTGACTTAAGATA 480
QY 161 LysCysGluProlysGluGlySerIleProleuLeuYrglurpGlnlysIleSerAsn 180
Db 481 ARATGTGAAACCAGAAAGAGGTCACTTCATTCAGATGAGGGCAGAAATGGCTGAC 540
QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerVallys 200
Db 541 TCACAGAAATGCCACTTCAGGTTAGCAGAAATGACTCATCTGTATATCTGTAAA 600
Db 201 AspAlaLysSerThrGluThrSerGlyThrThrSerCysThrValleuLysAsnArgValGlySer 220
Db 601 AACGCCCTCTCTGAGTACTCTGGACATACGTCAGTCAGAACAGAGTGGCTCT 660
QY 221 AspGlyCysLeuLeuArgLeuaspValValProProSerAsnArgAlaGlyThrLeala 240
Db 661 GATCAGTCCTGCTGCTGCTCTAACTCAATTAAGTGACTAATGCA 720
QY 241 GlyAlaValIleGlyValleuLeuAlaLeuValleuLysGlyLeuIleLepheCysCys 260
Db 721 GGAGCCATTATAGGAACTTGCCTGCTCTASCGCTCATGGCTCTATCATCTTTGCTG 780
QY 261 Arg 261
Db 781 CGT 783

RESULT 2
ID AAC85813 standard; cDNA; 2434 BP.
ID AAC85813
AC AAC85813;
XX
AC AAC85813;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human CAR cDNA.
XX
KW Coxsackie virus and/or Adenovirus receptor; CAR; transgenic mouse;
KW transgene; tCAR; transduction; integrin; gene transfer; lymphocyte;
KW lymphocyte-specific transcription regulatory sequence; T cell; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT FT
CDS 60..1157
FT /*tag= a
FT /product= "CAR"
XX
US6245966-B1.
XX
PD 12-JUN-2001.
XX
PF 19-MAR-1999; 99US-00927496.
XX
PR 14-JUL-1998; 98US-00927492.
XX
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PT Degregori J;
XX
WPI; 2001-366549/38.
DR DR
P-PSDB; AAB47270.
XX
PT Transgenic mouse comprising a nucleotide sequence encoding a truncated
PT Coxsackie virus and/or Adenovirus receptor (tCAR) polypeptide useful for
PT the analysis of cellular physiology -

PA (FERR/ FERRARA N.
PA (GERB/ GERBER H.
PA (GERR/ GERRITSEN M E.
PA (GODD/ GODDARD A.
PA (GODO/ GODOWSKI P J.
PA (GURN/ GURNEY A L.
PA (HILL/ HILLIAN K J.
PA (MARS/ MARSTERS S A.
PA (PANJ/ PAN J.
PA (PAON/ PAONI N F.
PA (STEP/ STEPHAN J F.
PA (WATA/ WATANABE C K.
PA (WILL/ WILLIAMS P M.
PA (WOOD/ WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Stephan JP, Gurney AL, Hillian KJ, Marsters SA, Pan J, Paoni NF; Williams PM, Wood WI, Ye W; DR; WPI; 2002-171999/22. P-PSDB; ABB95562.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal - Claim 1; Fig 279; 567PP; English.

CC The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.

XX Sequence 3059 BP; 1093 A; 559 C; 569 G; 837 T; 1 other; SQ Alignment Scores:

Pred. No.:	8.18e-123	Length:	3059
Score:	1238.00	Matches:	233
Percent Similarity:	94.25%	Conservative:	13
Best Local Similarity:	89.27%	Mismatches:	15
Query Match:	91.10%	Indels:	0
DB:	24	Gaps:	0

US-09-899-634C-2 (1-261) x ABL95700 (1-3059)

QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 77 ATGGCGCTCTGCGTGCTCTGCCTGCGAGGTGGATTTCGCCAGAGTTG 136
QY 21 SerIleThrThrProGluGlnMetIleGluGlyAlaLysGlyGluThrAlaTyrLeuPro 40
Db 137 AGTATCACTCTCTGAAGGAGATGATTGAAAGCAAGGGAAACTCCCTACTGCCA 196
QY 41 CysArgPheThrIleGlyProGluAspGlyGlyProLeuAspIleGluIleLeuSer 60
Db 197 TGCAGATTTCAGCTTAGTCGACAGCGGACGCCGCTGACATGAGGGCTGATACA 256
QY 61 ProAlaAspIleGlyIleValAspGlnValIleLeuTyrSerGlyAspIleSerIle 80
Db 257 CCAGGTGATTAATCAGAAGGGATCACGGATATTATATCTGGAGACAAATTAT 316
QY 81 AspAspTYrTyrgInAspLeuIleGlyIleValIleIlePheThrSerAsnAspLeuIle 100
Db 317 GATGACTACTATCCAGATCTGAAAGGCCGGTACATTTCAGTAATGCTCAATCT 376
QY 101 GlyAspAlaSerIleAsnValIleAspIleGlyIleValIlePheThrGlyIle 120
Db 377 GGTCATGCACTAACATAATGTAACGATTCAGCTGCAATATCAGTC 436

QY 121 LysValLysLeuAlaProGlyIvalGlyAsnLysLysIleGlnLeuThrValLeuLys 140
Db 437 AAAGTGAAGAAAGCTCCCTGGTGTGCAATAAGAAGATCCTGGAGATCTGTAAG 496
QY 141 ProSerGlyIlysArgCYSYTVAlaSArgGlySrglucuIleGlyAsnAspPhenylsIeu 160
Db 497 CCTCAAGTGCGAGATCTTACCTTGAGGATCTGAGAAATGGAATGACTTAAGATA 556
QY 161 LysCysGluProIysGluGlySerLeuProLeuLeuTyrgIutrgPheGlyIleSerAsn 180
Db 557 AAATGTCGACCAAGAGAGGTCACTTCATACAGTATGAGTGGCAGAAATGTCGAC 616
QY 181 SerGlyLysLeuProTrpLeuIlePheAlaGluMerThrSe-ProValIleSerValIys 200
Db 617 AACAGAAATGCCACTTCATGGTACAGTCAGAGAACAGACTGGCTCT 736
QY 201 AspGlyLysLeuLeuIleAglSerGlyIlysTyrSerCysThrValLeuSsArgValGlySer 220
Db 677 AAATGCCCTCTCTGAGTACTCTGGACTACAGCTGTCAGTCAGAACAGACTGGCTCT 736
QY 221 AspGlyLysLeuLeuIleAglSerGlyIlysTyrSerCysThrValLeuSsArgValGlySer 220
Db 737 GATCAGGCTCTGTCGCTCTAACGTCGTCCTCTAACATTAAGCTGGACTAATGCA 796
QY 241 GlyAlaValIleGlyValLeuLeuAlaIleLeuLeuIleGlyLeuIleIleHeCysCys 260
Db 797 GGAGCCATTATAGGACTTTGCTTGCTCTAGGCCTCATCTCATCTTTGCTGT 856

QY 261 Arg 261
Db 857 CGT 859

RESULT 6
XX ID AAD02924 standard; cDNA; 3060 BP.
XX AC AAD02924;
XX DT 31-MAY-2001 (first entry)
XX DE Human PRO5723 cDNA (DNA82361).
XX Human PRO5723 cDNA (DNA82361).
XX Human; PRO5723; antiinflammatory; dermato logical; immunosuppressive; antirheumatic; antiarthritic; osteopathic; anti anaemic; haemostatic; antithyroid; antidiabetic; antiviral; antipsoriatic; anti allergic; anti asthmatic; inhibitor; therapy; systemic lupus erythematosus; spondyloarthropathy; systemic sclerosis; systemic vasculitis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; autoimmune thrombocytopenia; immune mediated renal disease; hepatitis; demyelinating polyneuropathy; Guillain-Barré syndrome; Whipple's disease; hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis; inflammatory bowel disease; gluten sensitive enteropathy; skin disease; allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria; eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection; idiopathic pulmonary fibrosis; graft-versus-host-disease; ss.
OS Homo sapiens.

Key location/Qualifiers
CDS /*tag= a
/*product= "Human PRO5723 protein"
FT FT sig_peptide /*tag= b
FT FT mat_peptide /*tag= c
FT FT /*product= "Mature human PRO5723 protein"
XX PN WO200116319-A2.
XX PD 08-MAR-2001.
PP 23-AUG-2000; 2000WO-US23522.

Db 197 TCAATTAGCCTTACTCCGAAGCACCGGACCGCTGGACATCGAGTGGTGTATCA 256
 PR 99US-015173.
 PR 99WO-US2011.
 PR 99WO-US30095.
 PR 16-DEC-1999; 99WO-US30095.
 PR 257 CCAGCTGATAATCAGAAGGTGATCAGTGATTTATTCGGAGAACATTAT 316
 PR 01-MAR-2000; 2000WO-US05601.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US1305.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 05-JUN-2000; 2000US-0209832.
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Rumas D;
 PI Watanabe CK, Wood WI;
 XX WPI; 2001-226690/23.
 DR P-PSDB; AAY72878.
 XX
 PT New PRO polypeptides for treating immune related and inflammatory diseases such as rheumatoid arthritis, systemic vasculitis, asthma, autoimmune hemolytic anemia, and diabetes mellitus -
 XX
 PS Claim 2; Fig 9; 118pp; English.
 XX
 CC The present sequence is a cDNA (DNA82361 clone) encoding PRO5723 protein, PRO protein, its agonist or antagonist or its antibody which are capable of enhancing or inhibiting the proliferation of T-lymphocytes or of increasing the infiltration of inflammatory cells into a tissue are useful in the diagnosis and treatment of immune-related diseases in mammals. The PRO protein is useful for treating systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, Juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobilary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin disease such as bullous skin disease, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonia, idiopathic pulmonary fibrosis, hyper-sensitivity pneumonitis, transplantation associated diseases such as graft rejection or graft-versus-host-disease.
 XX Sequence 3060 BP; 1094 A; 559 C; 569 G; 837 T; 1 other;
 XX
 Alignment Scores:
 Pred. No.: 8.19e-123
 Score: 1238.00
 Percent Similarity: 94.25%
 Best Local Similarity: 89.27%
 Query Match: 91.10%
 DB: 22
 US-09-899-634C-2 (1-261) x AAD02924 (1-3060)
 QY 1 MetAlaLeuIeuLeuCYPhcValLeuIeuCYGlyValAlaAspLeuThrArgSerLeu 20
 QY 21 SerIleThrThrProGlnGlnMetIleGluIleGluThrAlaTyroLeuPro 40
 QY 77 ATGCCGCTCCTGCCTGCTGCTCTCCGAGTAGTGATTCGCCAGAGTTG 136
 Db Human PRO5723 nucleotide sequence SEQ ID NO:504.
 DE Human; secreted and transmembrane protein; PRO; cytostatic; KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing; KW diagnostic assay; ss.
 XX OS Homo sapiens.
 XX PN WO20073454-A1.
 XX PD 07-DEC-2000.
 PR 30-MAR-2000; 2000WO-US08439.
 XX 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-014107.
 PR 07-JUL-1999; 99US-014308.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-014936.
 PR 15-SEP-1999; 99WO-US21547.
 PR 15-SEP-1999; 99US-015863.
 PR 08-OCT-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 02-MAR-2000; 2000WO-US05004.
 PR 15-MAR-2000; 2000WO-US0581.
 PR 20-MAR-2000; 2000WO-US06884.
 PR XX
 PA (GETH) GENENTECH INC.
 XX
 PT Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PT Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PT Grimaldi CJ, Gurney AL, KJavlin IJ, Napier MA, Pan J, Paoni NF;
 PT Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 WPI: 2001-032160/04.
 DR P-PSDB; AAB65294.
 XX
 PRO poly nucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 2; Fig 317; 935pp; English.
 XX
 The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF4470 to AAF4470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF4087 to AAF4269 and
 CC AAB6514 to AAB6530 represent PCR primers and protein
 CC sequences given in the exemplification of the present invention.
 XX
 Sequence 3060 BP; 1094 A; 559 C; 569 G; 837 T; 1 other;
 SQ
 Alignment Scores:
 Pred. No.: 8 19e-123
 Score: 1238.00 Length: 3060
 Percent Similarity: 94.25% Matches: 233
 Best Local Similarity: 89.27% Conservative: 13
 Query Match: 91.10% Mismatches: 15
 DB: 22 Indels: 0
 Gaps: 0
 US-09-899-634C-2 (1-261) x AAF44263 (1-3060)
 QY 1 MetAlaLeuIleLeuCyspheValLeuCysGlyValAlaAspLeuThrArgSerLeu 20
 Db 77 ATGGCGCTCTGCGTCGTCGCTCCAGTGGAGATTGCCAGAGTT 136
 QY 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluIleAlaTerLeuPro 40
 Db 137 AGTATCACTACTCCGGAAGGAGATGATGAAAGCCAAAGGGAACTGCTATCTGCA 196
 QY 41 CysArgPheThrLeuGlyProGluaspGlyProleuaspIleGluTrpLeuLeu 60
 PR 197 TGAATTTCACCTTACGGCCAGAGCAGGACCCGGACCTGGACATCGGTGCTGATCA 256
 Db 61 ProAlaaspAspGlnlysValaspGlnValileIleneutrySerglyAspIleItyr 80
 PR 257 CCACTCTAAATCAGAGGGTGTCACTGATTTATTCCTGGAGCAATTAT 316
 QY 81 ASPASPYTYrglnapleuLysGlyArgvalIhsPheThrSerasnaspIleYser 100
 PR 317 GATGACTACTATCCAGATCTGAAAGGCGCAGTACATTCTACGATATGATCTCAAATCT 376
 PR 101 GLYASPLAaserIleasnValthrAspIeGlnLeuSeraspIleGLYThrTyrglnCys 120
 PR 377 GGTGATCATCATAATGtaGAAATTAAGTCACTTCAGATTCGACATATCAGTC 436
 Db 121 LysValIysLysAlaProglvIvalGlyAsnlysValIysValIeGlnLeuThrValIeUlys 140
 PR 437 AAAGTGAAAGCTCTGGTGTGCAATAAGAAGGTCATCTGGTAGTCATCTGGTAGTC 496
 Db 141 ProSerGlyThrArgCysTyvalAspGlySerGluGluIleGlyAsnAspHeYsIeu 160
 PR 497 CCHTCAGTCAGTGCAGATGTTACCTTGATGGATCTGAAAGAATGGTACATCTCAAACT 556
 PT 161 LysCysGluProIysGluGlySerLeuProIeLeuIeRgutUrpglnIysLeuSerAsn 180
 PT 557 AAATGTCGACAAAGAGGTTCACTTCATACATAGTACTGCGAAATGTCGAC 616
 PI 181 SerGlyIysLeuProThrIleupIeupIealagIumeetThrSerProvalIeserValIys 200
 DR 617 TCAAGAAATGCCACTTCATGGTACGAGATGTCATCTGGTACGTCGAA 676
 DB 201 AspAlaSerThrghlTuGlySerGluGluIleGlyAsnAspHeYsIeu 160
 PR 677 AATGCCCTCTCAGTACTCTGGACATACAGCTGTCAGAACAGACTGGCTCT 736
 PT 221 AspGlyGlySerLeuLeuIaGlyLeuaspValValProProSerAspArgIaLgIThrIleAla 240
 DB 737 GATCAGTCGCTCTGCTAAACGTTGTCCTCCCTCAATAAGCTGGACTAATGCA 796
 PR 241 GlyAlaValIleGlyIvalLeuLeuAlaIeLeuLeuIleGlyLeuIleIlePheCysCys 260
 PT 797 GGAGCCATITAGGAACCTTGTTGCTCTAGGCCTCTGGCTCTTCATCTTGGTGT 856
 DB 261 Arg 261
 PR 857 CGT 859
 PT RESULT 8
 ID AAC91489 AAC91489 standard; cDNA; 3060 BP.
 XX AAC91489;
 AC AAC91489;
 DT 21-MAR-2001 (first entry)
 XX DE Human PRO5723 cDNA.
 XX Human PRO5723 cDNA.
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
 KW antirheumatic; cardiotropic; antianaemic; immunosuppressive; antithyroid;
 KW antidiabetic; nootropic; neuroprotective; hepatotoxic; virucide;
 KW antiallergic; antiasthmatic; immune related disorder; ss.
 KW hepatobiliary disease; autoimmune disease; allergy; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO200073452-A2.
 XX PD 07-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-US15264.
 XX PR 02-JUN-1999; 99WO-US12252.
 PR 20-JUL-1999; 99US-0144732.

PR 20-JUL-1999; 99US-0144758.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

PR 09-DEC-1999; 99US-0170262.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PA (GETH) GENENTECH INC.

PR PA; 2001-025253/03.

XX PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

PI Hebert C, Henzel W, Kabakoff RC, Sheldon DL, Tunas D, Watanabe CK;

PI Wood WI;

XX DR P-PSDB; AAB50930.

PT Thirty three nucleic acids encoding PRO polypeptides which are useful

PT in the diagnosis and treatment of immune related disorders, e.g.

PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

PT thyroiditis and diabetes mellitus -

PS Claim 48; FIG 57; 218pp; English.

XX CC The present sequence is one of thirty three nucleic acids encoding PRO

CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and

CC antagonists are useful for treating and diagnosing immune related

CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems (such as multiple sclerosis, idiopathic

CC demyelinating polyneuropathy or Guillain Barre syndrome, and chronic

CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases

CC (such as infection, autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),

CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's

CC disease, autoimmune or immune-mediated skin diseases (such as bullous

CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC food hypersensitivity and urticaria), immunological diseases of the

CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis

CC and hypersensitivity pneumonitis), transplantation associated diseases

SQ Sequence 3060 BP; 1094 A; 559 C; 569 G; 837 T; 1 other;

Alignment Scores:

Pred. No.: 8.19e-123

Score: 1238.00

Percent Similarity: 94.25%

Best Local Similarity: 89.27%

Query Match: 91.10%

DB: 22

US-09-899-634C-2 (1-261) x AAC91489 (1-3060)

QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20

DB 77 ATGGCGTCCTCTGCTCTGCTCTGCGAGTAGTGATTTGCCAGAAGTTG 136

QY 21 SerIleThrThrProGluGlnMetIleGluLysAlaTysGlyLuthAlaTyRLeuPro 40

DB 137 AGTATCTACTCTGAGAGTAGATGATGAAAGAACGGCAAGGGAAACTGCCATC 196

QY 41 CysBargPheThrLeuglyProGluAPGGLyProLeuApileGluTrPheLeuSer 60

DB 197 TCGAAATTACGCTTACTCCGAAGACGACGGACCGCTGGACATCGAGGTGATTC 256

QY 61 ProAlaAspAspGlnLysValAspGlnValleleutyrSerGlyAspLysileTYR 80

DB 317 GATGACTACTATCCAGTCAGTGTGATCAAGTATTATTCGGAGACAATTAT 316

QY 101 GlyAspAlaSerIleLeuValThrAsnLeuSerAspIleGlyThrTyrglnCys 120

DB 377 GGTGATCCTACATAAATGTAAGANTTACACTGTCAGATATTGCGCACATATCAGTC 436

QY 121 LysValLysIleAlaProGlyValGlyAsnLysValleleutyrSerGlyAspLysileSer 100

DB 317 AAATGTGAAAAGCTCTGGCTTGCAATAGAGTTCATCTGGTAGTTGTTAG 376

QY 141 ProSerGlyThrArgCysTrpValAspGlySerGluGluLysAspPhenylsieu 160

DB 497 CCTTCAGCTGCGAGATGTTACCTGTTACAGTCACTGTCAGTCACTGTTGAG 556

QY 161 LysCysGluProLygsglyValgylasnyValleleutyrSerGlyAspLysileSer 180

DB 437 AAATGTGAAAAGCTCTGGCTTGCAATAGAGTTCATCTGGTAGTTGTTAG 496

QY 181 SerGlnLysIleProThrLeuTripleValAlaGluMetThrSerProValleleutyr 200

DB 617 TCACAGAAAATGCCACTTCATGGTTAGCAGAAATGACTCATCTGTCAGTC 616

QY 201 AsnAlaSerIleThrGluThrSerGlyAspLysValleutyrSerGlyAspLysile 220

DB 677 AMGCCCTTCCTGAGTCATCTGGACATACAGTCAGTCAGAAGACAGTGGCT 736

QY 221 AspGlnCysLeuLeuValGlyLeuAspValProProSerAsnArgAlaGlyThrIleAla 240

DB 737 GATCAGTCCTGTTGCCTCAAATAAAGCTGAACTGCA 796

QY 241 GlyAlaValleGlyValleuAlaLeuValleuLeuLeuLeuPheCysCys 260

DB 197 GGAGCCATTATGGAACTTGCTGCTCTAGGCCTCTGGCTTACATCTTGTG 856

QY 261 Arg 264

DB 857 CGT 859

RESULT 9 ARK33643

ARK33643 standard; cDNA; 3060 BP.

XX TD ARK33643;

XX AC ARK33643;

DT 08-MAY-2002 (First entry)

XX DE cDNA encoding human PRO protein, Seq ID No 215.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

XX breast cancer; prostate tumour; rectal tumour; liver tumour;

XX pericyte cell proliferation; chondrocyte cell proliferation;

XX tumour necrosis factor-alpha; gene; ss.

XX

PD XX 15-MAR-2001.

DB 835 AAGTGAAAGAAGCTCCCTGGTGTGCAATAAGAGATCATCTGGAGTCCTGTGTAAG 894

XX 01-SEP-2000; 2000WO-US24199.

QY 141 ProsergylThargCystYrralAspGlySrgLguLlglyAsnaspHelysleu 160

PR 03-SEP-1999; 99US-0152547.

PR 16-MAR-2000; 2000US-0190347.

PR 21-MAR-2000; 2000US-011321.

PR 31-MAY-2000; 2000US-0208382.

PR 20-JUL-2000; 2000US-0220467.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Thompson P, Lillie J;

XX WPI; 2001-211428/21.

PT Detection, assessment, prevention and therapy of ovarian cancer comprises detecting changes in the expression of a variety of markers -

PS Claim 1; Page 1181-1182; 1198pp; English.

CC The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (I) (see AAF9854 to AAF9730), in a patient sample, and (2) the normal level of expression of (I) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have cytostatic activities and can be used in antisense gene therapy. The methods, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF9853 to AAF9853 represent human kinase marker primers and probes which are used in the exemplification of the present invention.

XX Sequence 3276 BP; 995 A; 557 C; 660 G; 1053 T; 11 other;

Alignment Scores:

Pred. No. :	9e-123	Length:	3276
Score:	1230.00	Matches:	233
Percent Similarity:	94.25%	Conservative:	13
Best Local Similarity:	89.27%	Mismatch:	15
Query Match:	91.10%	Indices:	0
DB:	22	Gaps:	0

US-09-8999-634C-2 (11-261) x AAF98715 (1-3276)

QY 1 MetAlaLeuLeuLeuCysPheValLeuCysGlyValAlaLysLeuThrArgSerIeu 20

DB 475 ATGGCGCTCTGGCTGGCTGTCCTCTGGCTGGAGTAGTGGATTCCCGAGAGTTG 534

QY 21 SerIleth-ThrProGluGlnMetIleGluIlysAlaIysGlyGluIhsAlaTyroLeuro 40

DB 535 AGTTCTACTCTCTGGAAGAGATGATGTTGAAACGCCAACGGAACTGCCTACTGCCA 594

QY 41 CysArgPheThrIleGlyProGluAspGlyGlyProLeuAspIleGluTrpLeuLeu 60

DB 595 TGCCTAAATTCTTACGCTTAGTCGCCGAAACAGGGACGCTGACATGGCGTATCCA 654

QY 61 ProIleAspAspGlnGlnIysValAspGlnValIleLeuIleLeuIleLeuIleLeuIle 80

DB 655 CCACCTGATATCAGGAGGTGGATCAAAGTATTTATCTGGACACAATTAT 714

QY B1 AspAspPtyTyrGlnIysAspLeuIleGlyArgValIhsIlePheThrSerAspLeuIle 100

DB 715 GATGCTATATCTCCGATCTGAGGCGGAGTACATTAGCTAGCATGTCATACTCCAACT 774

QY 101 GlyAspAlaSerIleAsnValThrLeuIleGlnIleSerAspIleGlyIhsIlePhe 120

DB 775 GGTGATGCACTCAATTAATGATCACACTGTCAGATATGGCACATACTGGC 834

XX 121 LysValIlysIysAlaProGlyValGlyAanlysIlysIleGlnIeuthrValLeuIlys 140

DB 161 DycysGluProGlyGluGlyAspIleLeuLeuProLeuLeuYrglrrpGlyIysIeuseSerasn 180

QY 955 AATGTGAAACCAGAGAGGTACTTCCATTCAGTRGAGTGAATGGCANAATGTCGAC 1014

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

DB 181 SergInlysteLeuProIleLeuIleAlaGluMetIhsSerProValIleSerIvallys 200

QY 1015 TCAGAGAAATGCCCACTCATGGTTAGCAGAAATGACTCTCATCTGTGAAATGTCGAA 1074

DB 201 AsnAlaSerThrGluTrsSerGlyThrTyrSerCysThrValIlysAsnArgValGlySer 220

QY 241 GVALAVALLIIGLYVALIeLeuVALIeLeuVALIeLeuVALIeLeuVALIeLeuVALIe 260

DB 1195 GGAGCCATTATAGGAACTTTGGCTGCTCTAGGCTCATGGCTTATCATCTTTGCTG 1254

QY 261 Arg 261

DB 1255 CGT 1257

RESULT 11

ABV25520

ID ABV25520 standard; cDNA; 3963 BP.

XX AC ABV25520;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 25511.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PR 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 23-MAY-2000; 2000US-207454P.

PR 03-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endge WO, Monahan JE;

DR WPI; 2001-62795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 5079-5080; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the

us-09-899-634C-2.rng

Alignment Scores:
 pred. No.: 1.05e-121
 Score: 1.24.00
 Percent Similarity: 93.87%
 Best Local Similarity: 88.89%
 Query Match: 90.07%
 DB: 19

US-09-899-634C-2 (1-261) x AAV28845 (1-1584)

Qy 1 MetalalauLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
 Db 60 ArgGCGCCTCCCTGCTCTGCTGGAGTAGTGCAGAGTTG 119
 Db 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyRLeuPro 40
 Db 120 AGATCACTCTCTGAAGAGATGATGATGAAAGCCAAATGCCATCTGCCG 179
 Qy 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpIleLeu 60
 180 TCCAATTTCAGCTAGTCCCGAGACCAAGGCGCATCGACATCGAGTGCGTGATATCA 239
 Qy 61 ProIalaAspGlnGlyValAspGlnValleIleLeuTyRArgYasPheIleTyR 80
 Db 240 CCGCTGTATACAGAGCTGAAAGCCAGAACATCTGAGCAATTAT 299
 Qy 81 AspAspTVTYrgInAspLeuIgYargValHisPheThrSerAspAspIleYsser 100
 Db 300 GATGACTACTATCCAGATCTGAAAGCCAGAACATCTGAGTAATCTCAACT 359
 Qy 101 GLYASPAIaserLeuAsnValThrAspLeuGlnLeuUserAspIleGlyThrArgCys 120
 360 GGTGATGCACTAAATGTAACGATTCACACTGTCAGATAATGCCACATATCAGNC 419
 Qy 121 LysValIlysIyslaProGlyValGlyAsnIlysIleGlnLeuThrValLeuIys 140
 Db 420 AAATGTGAAAAAAGCTCTGGTGTGCAAATMAGAAGATCCTGGTAGTCCTGTAAAG 479
 Qy 141 ProSerGlyThrArgCysTyrvAlaSpaGlySerGluGluIleGlyAsnSpheLeu 160
 Db 480 CCTCAGGTGGAGATGTTACGTGATGCAAGAAATGGAAAGGCACTTAAGATA 539
 Qy 161 LysCysGluProIysGluGlySerLeuProLeuLeuTyrgLrpGlnIysLeuSerAsn 180
 Db 540 AAATGTGACCAAAAGAAGGTTCACTTCATACAGTAGTGGCAAAATGTGTCGAC 599
 Qy 181 SerGlnIysLeuProThrLeuIlePheLeuIgLuMetThrSerProValIleSerValIys 200
 Db 600 TCACAGAAATGCCACTTCATGTTACAGAAATGACTTCATCTGTATCTGTAAA 659
 Qy 201 AsnIleSerThrGluTyrsErGlyThrTyrsSerCysThrValIysAsnArgVAlgySer 220
 Db 660 AATGCCCTCTCTGAGTACTCTGGCACATACAGCTGAGCTGAGTCAGAACAGGGCTCT 719
 Qy 221 AspGlnCysLeuLeuLeuArgLeuAspValValProProSerAspArgAlaGlyThrIleAla 240
 Db 720 GATCAGTGCCCTGTTGCGCTAACTGTTGCGCCCTCTCAATAAGCTGGACTAAATCA 779
 Qy 241 GlyValAlaIleGlyValLeuLeuLeuLeuLeuIleGlyLeuIleLeuLeuCysCys 260
 Db 780 GGAGCCATTATAGGAACTTGCTTGCTCTAGCCCTCATGGCTTAATCATCTTGCTG 839
 Qy 261 Arg 261
 Db 840 CGT 842
 RESULT 13
 AAV28846
 ID AAV28846 standard; DNA; 1128 BP.
 XX AAV28846;
 AC AAV28846;

OS OS
 XX XX
 FH Key Location/Qualifiers
 FT CDS 1..1128
 /tag= "coxsackievirus and adenovirus receptor"
 /product= "coxsackievirus and adenovirus receptor"
 /transl except= "(pos:1096..1098,aa:Xaa)"
 /note= "Xaa= a stop codon, the sequence is shown as continuing but gets unclear"
 FT XX
 PR XX WO9811221-A2.
 DR XX 19-MAR-1998.
 PD XX 12-SEP-1997; 97WO-US16189.
 PT XX PR 13-SEP-1996; 96US-0026100.
 PA XX (DAND) DANA FARMER CANCER INST INC.
 XX PI Bergelson JM, Finberg RW, Horowitz MS;
 XX DR WPI; 1998-207384/18.
 DR P-PSDB; AAW57213.
 PT XX DNA encoding coxsackievirus and adenovirus receptor - useful for modulation of e.g. cardiac, pancreatic or gastrointestinal infection
 RS XX Disclosure; Fig 14; 104pp; English.
 CC The present sequence encodes mouse coxsackievirus and adenovirus receptor (CAR). The present invention also describes: (1) a method for modulating CAR expression comprising contacting the cell with an agent which modulates CAR protein activity or CAR nucleic acid expression, such that a cell associated activity is altered relative to a cell associated activity of the cell in the absence of the agent; and (2) a method for detecting the presence of CAR in a biological sample comprising contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected.
 CC Modulation of CAR is useful for treatment of cardiac infection, e.g. myocarditis, pericarditis or dilated cardiomyopathy, or infection of the central nervous system, e.g. a non-specific febrile illness or meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis, or infection of the respiratory or gastrointestinal tract or childhood onset diabetes mellitus. Probes derived from CAR nucleic acids are useful for hybridisation assays, and antibodies raised against CAR protein are useful for blocking CAR expression. Cell-free assays which include combining CAR protein and a candidate test compound are useful in screening for drugs which interact with CAR protein.
 CC Sequence 1128 BP; 297 A; 286 C; 288 G; 257 T; 0 other;
 SQ XX Alignment Scores:
 Pred. No.: 4.76e-121 Length: 1128
 Score: 1216.00 Matches: 229
 Percent Similarity: 93.85% Conservative: 15
 Best Local Similarity: 88.08% Mismatches: 16
 Query Match: 89.48% Indexes: 0
 DB: 19 Gaps: 0
 US-09-899-634C-2 (1-261) x AAV28846 (1-1128)
 Qy 1 MetalalauLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20

Db 1 ATGGCGGCCTACTGTCCTCGCTCTGTCGGGATTCACACTGGTTG 60 PF 30-JAN-1998; 98WO-US01724.
 QY 21 SerileThrThrProGluGlnMetIleGluLysAlaValGlyGluThrAlaLeuPro 40 XX PR 30-JAN-1997; 97US-0036986.
 Db 61 AGCATCACTACACCGAAAGAGGTGAAAGAACGAAAGGGAAACTGCGTATCTACA 120 XX PA (UNY) UNIV NEW YORK STATE.
 QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluThrLeuSer 60 XX PI Philipson L, Tomko RP;
 Db 121 TGCAGTTTACTCTCAGTCCGAGACGAGGACACTGAGCATTAAGTGCGATATCC 180 DR XX WPI; 1998-437397/37.
 QY 61 ProLaAspAsnGlnLysValAspGlnValIleLeuTySerGlyAspLysIleTyr 80 XX P-PSDB; AAW69698.
 Db 181 CCGCTGATAACAGATAGTGGTCAAGTGCATTTGATCTGGAGACAAATTAT 240 PT DNA encoding human receptor for adenovirus and coxsackievirus B -
 QY 81 AspAspPheTyrGlnAspIleLysGlyArgValHisPheThrSerAspIleLysSer 100 XX for preventing and treating viral infection and rendering cells
 susceptible to transformation by adenoviral vectors in gene therapy
 Db 241 GATAACTACTATCCGGATCTGAAGGACGGTACATTAGAGTAACGATGTCAGCT 300 PS Claim 2; Page 68-70; 88PP; English.
 QY 101 GlyAspAlaSerIleAsnValThrAsnIleGluLeuAspIleGlyPheGlyThrGly 120 CC This cDNA molecule codes for mouse NCAR protein (see AAW69698) that
 301 GGCGACGCATCTAAATGTCGACCAACCTGCACTGCGACATGGCACTTACAGTC 360 CC serves as a cellular receptor for adenoviruses of the serotypes 2
 and 5 (subgroup C) and for the group B coxsackieviruses (CVB). It
 421 CCTCAGGTACAAGATGCTCGTGGATGGAAATGACTCAAGTA 480 CC was obtained by screening a lambda phage expression cDNA library
 with antisera containing antibodies specific for mouse CVB
 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGluLeuThrValLeuLys 140 CC binding protein p46, and was used to identify human HCAR cDNA
 361 AAGTGAAGAAGCCCTGGGTTGCAATAAGAAATTCTGGTGAGCTCTGGTAAG 420 CC (see AAV5029). The invention also provides host cells transformed
 141 ProSerGlyThrArgCYtPheYrValAspGlySerIleGluIleGlyAspAspPheIle 160 CC with DNA molecules encoding HCAR or NCAR and methods of producing
 421 CCTCAGGTACAAGATGCTCGTGGATGGAAATGACTCAAGTA 480 CC their recombinant proteins or their derivatives. These proteins,
 161 LysCysGluProDysGlyGlySerIleProLeuLeuTyRgluTrpGlyLysIleSerAsn 180 CC their extracellular domains, as well as oligopeptides (see
 481 AAATGTGACCAAGCGCTCCACTACAGTTGATGGCAGAACATGTCGGAC 540 CC AAW69697-708) which bind virus, are also provided. Isolated HCAR or
 181 SerGlnLysIleProThrLeuTpleuAlaGluMetThrSerProValIleSerValLys 200 CC NCAR proteins or their fragments or variant are used to prevent
 541 TCCGAGACATGCTACGCCATGCTGGCAGAAATGACCTCACAGTATCTGGAG 600 CC these viral infections. Expressing the DNA in cells which lack
 201 AspIlaSerThrGluYrSerGlyLysThrTyrsSerCysThrValLysAsnArgValGlySer 220 CC or treat virus infections. Expressing the DNA in cells which lack
 601 AACGCCAGTCTGAGTATCTGGACATRAGTCGACGGTCACAAACAGTGGCT 660 CC these viral receptors renders the cells susceptible to gene
 221 AspGlnCysSerLeuIleArgLeuAspValIleProProSerAsnAaGlyGlyThrIleIla 240 CC transformation by adenoviral vectors carrying genes for gene
 661 GACCGTGTGTCGACTAGACGTTGTCACCCACCTCCACCGAGCCGACGATCGCG 720 CC therapy.
 QY RESULT 14 DB Sequence 1301 BP; 355 A; 327 C; 322 G; 297 T; 0 other;
 DB Alignment Scores:
 Pred. No.: 5.8e-121 Length: 1301
 Score: 1216.00 Matches: 229
 Percent Similarity: 93.85% Conservative: 15
 Best Local Similarity: 88.08% Mismatches: 16
 Query Match: 89.48% Indels: 0
 DB: 19 Gaps: 0
 US-09-899-634C-2 (1-261) x AAV50430 (1-1301)
 QY 1 MetalAlaLeuLeuCysPheValLeuCysGlyValAlaAspLeuThrArgSerLeu 200 DB 157 ATGGCGGCCTACTGTCCTCTGCGCTTCTGCGGGATTCGGGATTCACAGTGTTG 216
 QY 21 SerileThrThrProGluGlnMetIleGluLysAlaValGlyGluThrAlaLeuPro 40 DB 217 AGCATCACTACACCGAAAGAGGATGAAAGAACGAAACTGGATCTACCA 276
 ID AAV50430 standard; cDNA; 1301 BP.
 XX AAV50430; AC 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluThrLeuSer 60 DB 277 TGCAAGTTTACTCTCAGTCCGAGACGAGGACACTGGACATTGAGTGGTATCC 336
 XX DT 07-DEC-1998 (first entry)
 XX DR Mouse coxsackievirus and Ad2 and Ad5 receptor (MCAR) cDNA.
 XX KW MCAR: coxsackievirus receptor; CVB: adenovirus; Ad2 receptor;
 XX Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.
 OS Mus sp.
 XX Key Location/Qualifiers
 FH FT 157 .1215 QY 101 GlyAspAlaSerIleAsnValThrAsnIleGluLeuAspIleGlyGlyCys 120
 CDS FT /*tag= a. DB 457 GGGACTGATCTATAATGTCGACACTGCGACTGCGACTTACAGTC 516
 XX WO9833819-A1. PN QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys 140 DB 517 AAAGTGAAGAAGGCCCTGGGTTGCAATAAGAAATTCTGCTGACCGTCTGTTAG 576

QY 141 ProSerGlyThrArgCysTyValAspGlySerGluGluileGlyAsnAspPheLeu 160
 QY ||||| ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 577 CCTTCAGGCAAGATGCTTCGGATGGATCGGAAGAGATTGAAATGACTCAAGTA 636
 QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuThrGluTrpGlyLysLeuSerAsn 180
 QY ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 637 AATGTGAACTTACGCCATGGCTTCCACTACAGTTGAAATGGCAGAACCTGCGAC 696
 QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProLeuSerVallys 200
 QY ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 697 TCCGAGAACATGCCTACGCCATGGCTGGAGAAGATGAGTCACAGTTATGTGAG 756
 QY 201 AsnAlaSerThrGluThrSerGlyThrSerCysThrVallysAsnArgValGlySer 220
 QY ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 757 AACGCCAGHTCTGAGTATCTGGACATACAGCTGAGGTCAAACAGAGGGCTCT 816
 QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLeAla 240
 QY ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 817 GACCAGTGATGCTGGCAGTAGAGCTGTTGCCACCTCCACCCACGGAGGATCGG 876
 QY 241 GlyAlaValAlleGlyIgYValLeuAlaLeuValLeuIleGlyLeuIleIlePheCys 260
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 877 GGCCCCGTCATAGGAGCTGCTGCCCTGTGTCATCGGGCCATCTCTCTGCTG 936
 RESULT 15
 AAV72025 DT 29-MAR-1999 (first entry)
 ID AAV72025 standard; DNA; 795 BP.
 XX AC AAV72025;
 XX Adenovirus PACTSG2-SCAR DNA.
 KW PACTSG2-SCAR; chimeric protein; adenoviral fibre protein; monomer; trimerisation domain; affinity; substrate; gene therapy vector; attachment; interaction assay; infection; ss.
 OS Mastadenovirus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..795 /tag= a /product= "PACTSG2-SCAR" /note= "chimeric protein"
 FT W09854346-A1.
 XX PR 03-DEC-1998.
 XX PR 28-MAY-1998; 98W0-US11024.
 XX PR 16-JAN-1998; 98US-0071668.
 XX PR 28-MAY-1997; 97US-0047849.
 PA (GENV-) GENVEC INC.
 XX PI Brough DE, Binfield D, Kovessi I, Lizonova A, Roslalink PW;
 PI Wickham TJ, Yonehira G;
 XX DR WI; 1999-059848/05.
 DR P-PSDB; AAWB2729.
 PT New adenoviral fibre trimer with reduced binding to native substrate - useful for, e.g. preparing gene therapy vector with minimal ectopic infection for in vitro applications
 Example 8; Page 58-59; 103pp; English.
 XX CC This sequence encodes a novel adenovirus chimeric protein, PACTSG2-SCAR.

CC having an N-terminus of an adenoviral fibre protein and a trimerisation domain. Such monomers have lower affinity for native substrate than the native adenoviral fibre trimer. Cell lines containing such monomers are used (i) to propagate adenovirus for use as gene therapy vectors (for in vitro or in vivo applications, (ii) as reagents for studying adenoviral attachment and infection, and (iii) in receptor-ligand interaction assays. The new viruses produce minimal ectopic infection (they can not infect native host cells) so are safer as vectors and can be engineered for selective targeting to other cells.

XX Sequence 795 BP; 236 A; 157 C; 191 G; 211 T; 0 other;

Alignment Scores:
 Pred. No.: 2.67e-113 Length: 795
 Score: 1142.00 Matches: 214
 Percent Similarity: 94.63% Conservative: 15
 Best Local Similarity: 88.43% Mismatches: 13
 Query Match: 84.03% Indels: 0
 DB: 20 Gaps: 0

US-09-899-634C-2 (1-261) x AAV72025 (1-795)

QY 1 MetAlaLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
 Db 1 ATGGCGCTCCCTCTGCTCTGCTCTGCTGCGGACTAGTGATTTGCCAGAAAGTTG 60
 QY 21 SerLeuThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaIleLeuPro 40
 Db 61 AGTATCACTACTCTGAGAGATGATGAAAAAGCCAAAGGGAAACTGCCATCTCCG 120
 QY 41 CysArgGlyThrLeuGlyProGluAspGlyProLeuAspIleGluIleLeuLeuSer 60
 Db 121 TGCACATTACGCTTAGTCCCAGAACGACAGGACCGTGGACATCGGGTGTATCA 180
 QY 61 ProAlaAspGlnLysLeuAspGlnValIleLeuLeuThrSerGlyAspLysIleTyr 80
 Db 181 CCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTATCTGAGACAATTAT 240
 QY 81 AspAlaSpTyTyGlnAlaLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
 Db 241 GATGACTRACTATCCAGTCAGTCAGTGAAGAGCCGAGTCATTACAGTAATGACTAATCT 300
 Db 101 GLYAspAlaSerIleAlaValThrAsnLeuGlnLeuSerAspIleGlyThrGlyCys 120
 Db 301 GGTTGATCCTCATATAATGTAAGCAATTACACTGTCAGATATTGCCACATATCACGCC 360
 QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys 140
 Db 361 AAAGTGGAAAAGCTCTGGGTTGCAATAGAAGATTCACTGGTGAAGTCCTGTAAG 420
 QY 141 ProSerGlyThrArgCysTyValAsnLysGlySerGluGluileGlyAsnAspPheLeu 160
 Db 421 CCTTCAGSTGGAGATTTACGTGATGAGATCTGAGAAATTGGAAAGTGACTTAAGATA 480
 QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuThrGluTrpGlyLysLeuSerAsn 180
 Db 481 AATGTGAACTTACGCCATGGCTTCCACTACAGTTGAAATGGCAGAACATTGCTGAC 540
 QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProLeuSerVallys 200
 Db 541 TCCAGAAATGCCACTTCATGGTTGCAAGAATGCTTCATCTGTTATATCTGTAAGA 600
 QY 201 AsnAlaSerThrGluThrSerGlyThrSerCysThrVallysAsnArgValGlySer 220
 Db 601 AATGCCCTCTGAGTCATCTGGACATACGTGAGTCAGTCAGTCAGTCAGTCAGTCAGTC 660
 QY 221 AspGlnCysLeuLeuAspLeuAspValValProProSerAsnArgAlaGlyThrLeAla 240
 Db 661 GATCAGTCCTGTCGCTCTCAAAACGTTGTCCTCTCAAAAGCTGGATCCTGAGTC 720
 QY 241 GlyAla 242
 Db 721 GGCTCA 726

Wed Jul 16 14:24:18 2003

us-09-899-634a-2.rng

Page 16

Search completed: July 12, 2003, 12:09:32
Job time : 194 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 12:03:42 ; Search time 45 Seconds
(without alignments)

1778.725 Million cell updates/sec

Title: US-09-899-634C-2
Perfect score: 1359

Sequence: 1 MALLICFVLLCGVADLRLS..... AVIGVLLALVLGLIIFCCR 261

Scoring table: BL0SUM62

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Ygapext 10.0 , Ygapext 0.5
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Delop 6.0 , Delect 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7
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Database : Issued_Patents_NA:*

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6: /cgn2_6/ptodata/1/ina/backfiles.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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RESULT 1
US-09-272-496-1
; Sequence 1, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: DeGregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09-272,496
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KSY: CDS
; LOCATION: (60)..(1154)
US-09-272-496-1

ALIGNMENT SCORES:
Pred. No.: 7.3e-144
Score: 1238.00
Percent Similarity: 94.25%
Best Local Similarity: 89.27%
Query Match: 91.10%
DB: 4
Length: 2434
Matches: 233
Conservative: 13
Mismatches: 15
Indels: 0
Gaps: 0

US-09-899-634C-2 (1-261) x US-09-272-496-1 (1-2434)
Qy 1 MetAlaLeuLeuLeuGlyPheValIleLeuGlyValAlaAspLeuThrArgSerLeu 20
Db 60 ATGGCCTCCCTGCTCTGCTCTGCTGCTGCGGAGTAGTCGATTGCCAGAGTTG 119

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,383B
 FILING DATE: 12-SEP-1997
 CLASSIFICATION:
; ; ; ;
 PRIORITY APPLICATION DATA:
; ; ; ;
 APPLICATION NUMBER: US 60/026,100
 FILING DATE: 13-SEP-1996
; ; ; ;
 ATTORNEY/AGENT INFORMATION:
; ; ; ;
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
; ; ; ;
 REFERENCE DOCKET NUMBER: DFN-020
; ; ; ;
 TELECOMMUNICATION INFORMATION:
; ; ; ;
 TELEPHONE: (617) 227-7400
; ; ; ;
 TELEFAX: (617) 742-4214
; ; ; ;
 INFORMATION FOR SEQ ID NO: 3:
; ; ; ;
 LENGTH: 1095 base pairs
; ; ; ;
 SEQUENCE CHARACTERISTICS:
; ; ; ;
 TYPE: nucleic acid
; ; ; ;
 STRANDEDNESS: single
; ; ; ;
 TOPOLOGY: linear
; ; ; ;
 MOLECULE TYPE: cDNA
; ; ; ;
 FEATURE:
; ; ; ;
 NAME/KEY: CDS
; ; ; ;
 LOCATION: 1..1095
; ; ; ;
 US-08-928-383B-3
; ; ; ;
 Alignment Scores:
; ; ; ;
 Pred. No.: 1..12e-142 Length: 1095
; ; ; ;
 Score: 1224.00 Matches: 232
; ; ; ;
 Percent Similarity: 93.87% Conservative: 13
; ; ; ;
 Best Local Similarity: 88.89% Mismatches: 16
; ; ; ;
 Query Match: 90.07% Indels: 0
; ; ; ;
 DB: 4 Gaps: 0
; ; ; ;
 US-09-899-634C-2 (1-261) x US-08-928-383B-3 (1-1095)
; ; ; ;
 QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyYValAlaAspLeuThrArgSerLeu 20
; ; ; ;
 Db 1 ATGGCCGCCCTGCTGCGCTCTGCTGCTGCGCTGCGATTCAGTCAAGCTGGCGCT 719
; ; ; ;
 QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLeuAla 240
; ; ; ;
 Db 720 GATCAGTGCCGTGTCGCTTAACGTGTCGCCCTCAATAAGCTGACTATTCGA 779
; ; ; ;
 QY 241 GlyAlaValAlleGlyValLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuCys 260
; ; ; ;
 Db 780 GGACCCATTAACTGAACTTGCTGCTGCTGCGCTCATGGCTATCATCTTGCTG 839
; ; ; ;
 QY 261 ARG 261
; ; ; ;
 Db 840 CGT 842
; ; ; ;
RESULT 2
; ; ; ;
 US-08-928-383B-3
; ; ; ;
 Sequence 3, Application US/08928383B
; ; ; ;
 Patent No. 6210521
; ; ; ;
 GENERAL INFORMATION:
; ; ; ;
 APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; ; ; ;
 TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; ; ; ;
 NUMBER OF SEQUENCES: 26
; ; ; ;
 CORRESPONDENCE ADDRESS:
; ; ; ;
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
; ; ; ;
 CITY: Boston
; ; ; ;
 STATE: Massachusetts
; ; ; ;
 COUNTRY: USA
; ; ; ;
 ZIP: 02109
; ; ; ;
 COMPUTER READABLE FORM:
; ; ; ;
 MEDIUM TYPE: Floppy disk
; ; ; ;
 COMPUTER: IBM PC compatible

QY 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaThrLeuPro 40
; ; ; ;
 Db 120 AGFATCACTACTCTGAGAGATGATGAAAGCCAAGGGAAACGCCATCTGCC 179
; ; ; ;
 QY 41 CYArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuSer 60
; ; ; ;
 Db 180 TGCRAATTAGCTTAGTCCGAGAACAGGGACCGCTGACATCGAGTGCTGATCA 239
; ; ; ;
 QY 61 ProLalaAspGlnLysValAspGlnValLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
; ; ; ;
 Db 240 CCGAGCTGATAATCAGAAGCTGAGTTCAGTATTCAGTATTCAGTATTCAGTATCA 299
; ; ; ;
 QY 81 AspAspTYrYrgInAspLeuLysGlyArgValHisPheThrSerAspLeuSer 100
; ; ; ;
 Db 300 GATGACTACTATCCAGATCTGAGAAAGGCCAGTCATTTAGCTGAGTAATGATCCAACT 359
; ; ; ;
 QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuAspIleGlyThrIleGly 120
; ; ; ;
 Db 360 GGATGATGCACTAAATAATGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 419
; ; ; ;
 QY 121 LysValLysIleAspIleGlyAsnLysValAspIleGlyAsnLysValAspIleGly 140
; ; ; ;
 Db 420 AACATGAAATAAGCTCTGGTGTGCAATAAGAGATTCATCTGAGTCTGTTAG 479
; ; ; ;
 QY 141 ProSerGlyThrArgCysTyrrValAspGlySerCluGluIleGlyAspPheLeu 160
; ; ; ;
 Db 480 CCTTCAGGCGAGATGTTAGCTGATGCTGAGAACTGAGCTTAAGATA 539
; ; ; ;
 QY 161 LysCysGluProLysGluGlySerIleLeuProLeuLeuTyrrGluTrpGlyLysLeu 180
; ; ; ;
 Db 540 AAATGTAACAAAGAGGTCATCTCCATAGTGTAGTGGCAAAATGCTGAC 599
; ; ; ;
 QY 181 SerGlnLysIleProThrLeuTrpLeuAlaGlyAlaMetThrSerProValIleSer 200
; ; ; ;
 Db 600 TCACAGAAATGCGCACTCTAGCTGTTAGAGAATGACTCATGTTATCTGATAA 659
; ; ; ;
 QY 201 AspAlaSerThrGluTyrrSerGlyThrTyrrSerCysThrValIleAsnArgValGlySer 220
; ; ; ;
 Db 650 AATGCCCTCTCTGAGTACTCTGGACATACAGCTGAGCTGAGTCAGAAGCTGGCT 719
; ; ; ;
 QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLeuAla 240
; ; ; ;
 Db 720 GATCAGTGCCGTGTCGCTTAACGTGTCGCCCTCAATAAGCTGACTATTCGA 779
; ; ; ;
 QY 241 GlyAlaValAlleGlyValLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuCys 260
; ; ; ;
 Db 780 GGACCCATTAACTGAACTTGCTGCTGCGCTCATGGCTATCATCTTGCTG 839
; ; ; ;
 QY 261 ARG 261
; ; ; ;
 Db 840 CGT 842
; ; ; ;
RESULT 2
; ; ; ;
 US-08-928-383B-3
; ; ; ;
 Sequence 3, Application US/08928383B
; ; ; ;
 Patent No. 6210521
; ; ; ;
 GENERAL INFORMATION:
; ; ; ;
 APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; ; ; ;
 TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; ; ; ;
 NUMBER OF SEQUENCES: 26
; ; ; ;
 CORRESPONDENCE ADDRESS:
; ; ; ;
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
; ; ; ;
 CITY: Boston
; ; ; ;
 STATE: Massachusetts
; ; ; ;
 COUNTRY: USA
; ; ; ;
 ZIP: 02109
; ; ; ;
 COMPUTER READABLE FORM:
; ; ; ;
 MEDIUM TYPE: Floppy disk
; ; ; ;
 COMPUTER: IBM PC compatible

QY 81 AspAspTYrYrgInAspLeuLysGlyArgValHisPheThrSerAspLeuSer 100
; ; ; ;
 Db 241 GATGACTACTATCCAGATCTGAGAAAGGCCATCTGCCAACT 300
; ; ; ;
 QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuAspIleGlyThrIleGly 120
; ; ; ;
 Db 301 GGTGATCCTCATCAAATGTAACGAACTGAGTATGACATATCAGCTG 360
; ; ; ;
 QY 121 LysValLysIleAspIleGlyAsnLysValAspIleGlyAsnLysValAspIleGly 140
; ; ; ;
 Db 421 CCTTCAGGCGAGATGTTACGTGATGAGGATCTGAGAACTGACTTAAGATA 480
; ; ; ;
 QY 161 LysCysGluProLysGluGlySerIleLeuProLeuLeuTyrrGluTrpGlyLysLeuAsn 180
; ; ; ;
 Db 481 AAATGTAACAAAGAGGTCATCTGGCAAAATGCTGAC 540

QY 181 SerGlnLySleuProThrLeuTripleuAlaGluMetThrSerProValleSerVallys 200
Db 541 TCAAGAATAATGCCAACTTCATCGTTAGCGAAGTAGCTCATCTGTATATCGTAAA 600
QY 201 AsnAlaSerThrGluTySerGlyThrTyrSerCysThrValleuBasalValGlySer 220
Db 601 AATGCCCTCTTCAGTACTCTGCGACATCAGCTGACAGAACAGAGGGCT 660
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 661 GATCAGGCGCTGTTGCGTCAAACGTTGRCCTTCATAGCTGGACTTAATGCA 720
QY 241 GlyAlaValleuGlyValleuLeuAlaValleuLeuAlaValleuLeuAlaValleuLeu 260
Db 721 GGAGCCATTATAGGAACTTGCTTGCTCTAGGCCTCATGGCTTATCATCTTGCTG 780
QY 261 Arg 261
Db 781 CGT 783

RESULT 3
US-08-928-383B-1
; Sequence 1, Application US/08928383B
; Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A NO. 6210921el Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928, 383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/026, 1100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36, 207
REFERENCE DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 744-2114
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 60..1157
US-08-928-383B-1
Alignment Scores:
Pred. No.: 2.03e-142 Length: 1584
Score: 1224.00 Matches: 232
Percent Similarity: 93.8% Conservative: 13

RESULT 4
US-08-928-383B-2 (1-261) x US-08-928-383B-1 (1-1584)
Best Local Similarity: 88.89% Query Match: 90.07%
DB: 4 Gaps: 0
QY 1 MetAlaLeuLeuLeuCysPhValleuLeuCysGlyAlaValLeuAlaAspLeuThrArgSerLeu 20
Db 60 ATGGCGCTCCCTCTCTGCTCTGCTGCGGGTAGTGGATTGCCACAGTTG 119
QY 21 SerIleThrThrProGluGluMetIleGluLysAlaLysGlyGluThrAlaTyrLeuPro 40
Db 120 AGTATCACTACTCTGAGAGATGATGGAAGAACGCGTCTACTGCT 179
QY 41 CysArgPhethrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuSer 60
Db 180 TCCAAATTAGCTACTCCGAGACGAGAACGGAACTGCTCATCTGCG 239
QY 61 ProAlaAspArgGluLysValAspGlnValleuIleLeuThrSerGlyAspIleTyr 80
Db 240 CCAGCTGATAATCAGAGGTGATCAGTGTATTATTCGGACACAATTAT 299
QY 81 AspAspTYRTYRGlNAspLeuLysGlyArgValHisPhethrSerAsnAspIleUsser 100
Db 300 GATGACTACTATTCAGATCTGCTGAAGGCCGATCATTTACAGTA 359
QY 101 GlyAspAlaSerIleLeuAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGly 120
Db 360 GGTGATGCAUTATAATAATGTAAGTAACTGTCAGATATGGCACATATCAGTC 419
QY 121 LysValLysValProGlyValGlyAsnLysValGlyAsnLysValGly 140
Db 420 AAAGTGAAAAAGCTCTGGTTGCAATCTGCT 479
QY 141 ProSerGlyThrArgCYSValAspGlySerGluGluLysGlyAsnAspPhelyLeu 160
Db 480 CCTCAGGTGGAGAGCTAGTGTGGAACTGAGAATGGAGAATGGACTGCAATTAAGTA 539
QY 161 DsCYGluUProLYGluGlySerLeuProLeuTyGluTrpGlnLysLeuSerAsn 180
Db 540 AAATGIGAACCAAAGAGGAGTTCACTTCATTAACAGTATGACTGGCAAAATGTCAC 599
QY 181 SerGlnLySleuProThrLeuTripleuAlaGluMetThrSerProValleSerVallys 200
Db 600 TCAAGAATAATGCCAACTTCATCGTTAGCGAAGTAGCTCATCTGTATCTGTTAG 659
QY 201 AsnAlaSerThrGluTySerGlyThrTyrSerCysThrVallysAsnArgVallys 220
Db 660 AATGCCCTCTTCAGTACTCTGGACATACTGCTGACAGTGAAGAACGAGGGCT 719
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 720 GATCAGGCGCTGTTGCGTCAAACGTTGRCCTTCATAGCTGACTTAATGCA 779
QY 241 GlyAlaValleuGlyValleuLeuAlaValleuLeuAlaValleuLeuAlaValleuLeu 260
Db 780 GGAGCCATTATAGGAACTTGCTTGCTCTAGGCCTCATGGCTTATCATCTTGCTG 839
QY 261 Arg 261
Db 840 CGT 842

ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/928,383B
 FILING DATE: 12-SEP-1997
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: DFN-020

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1515 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1095
 DB: US-08-928-383B-25

Alignment Scores:
 Pred. No.: 1.87e-141
 Score: 1216.00
 Percent Similarity: 93.85%
 Best Local Similarity: 88.08%
 Query Match: 89.48%
 DB: 4

US-09-899-634C-2 (1-261) x US-08-928-383B-25 (1-1515)

QY 1 MetAlaLeuIeuLeuCysPheValIeuLeuCysGlyValAlaAspLeuThrArgSerIeu 20
 Db 1 ATGGCGGCTACTGTCTGCTCTTGCGGATGCCATTCAACAGTGGTTG 60
 QY 21 SerileThrProGluIglnMetIleGluIysValAlaGlyGluThrAlaTyLeuro 40
 Db 61 AGCATCACTAACCCGAAGGAGATCGAAAGGGAACTCGTAACTACA 120

QY 41 CysArgPheThrLeuGlyProGluAspGlyProLeuAspIleGluTrpLeuLeu 60
 Db 121 TGCAGTTPACTCTCAGTCGGACACTGGACATGAACTGGCTGATGCC 180

QY 61 ProAlaAspAsnGlnIysValAspIvnVilleIleLeuIvnYrSerGlyAspLeuIleTyr 80

Db 181 CGCTGTGATPACAGATAGTGGATCAAGTCATCTTGTGAGAACATTAT 240

QY 81 AspAspTYrGlnIasPheLeuGlyArgValHisPheThrSerAspLeuIysSer 100

Db 241 GATACTATATCCGGATGAGGACGGTAGATTCAGTCAGTCAGTCAGCT 300

QY 101 GlyAspAlaAspIleAsnValThrAsnIeuLeuAspIleGlyIvnTyrGly 120
 Db 301 GGCGACGCACTTAACTGACCAACCTGCGACSTGTCGACATGGCACTTACAGTCG 360

QY 121 LysValIvnIysAlaProGlyValGlyAenIysIleGlnIeuThrValLeuIys 140

RESULT 5
 US-08-597-495B-23
 ; Sequence 23, Application US/08597495B
 ; Patent No. 5712369

GENERAL INFORMATION:
 APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
 APPLICANT: Simpson, Richard J.; Nice, Edward; Moritz, R. L.;
 APPLICANT: Cattimel, B.; Ji, Hong; Burgess, Anthony W.;
 APPLICANT: Heath, Joan K.; White, Sam J.; Johnstone, Cameron
 TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Falle & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/597,495B
 FILING DATE: 02-Feb-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/511,876
 FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Hanan, No. 571269man D.
 REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5316.1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 838-3884

TELEFAX: (212) 688-9200

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
 LENGTH: 960 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-597-495B-23

Alignment Scores:

Pred. No.: 3.39e-34 Length: 960
 Score: 351.50 Matches: 89
 Percent Similarity: 54.41% Conservative: 53
 Best Local Similarity: 34.10% Mismatches: 96
 Query Match: 25.86% Deletions: 23
 DB: Gaps: 11

US-09-899-634C-2 (1-261) x US-09-068-495B-23 (1-960)

Qy 10 LeuCysGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluglnMetIle 29
 Db 34 CTCGTGAGTAGGGTGACCGTGCATGCCCTCTGGAACACTCCACCTCCAGT 93

Qy 30 GluLysAlaLysGlyGluThrAlaTyroLeuProCysArgPheThrLeuGlyProGluAsp 49
 94 CGGGCTTGCAGGAAAGAGTGTACCCCTGCCCTGACCTACACTCCACCTCCAGT 153

Qy 50 GlnglyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspIleGlnLys 66
 154 CGAGAGGCACT----ATCAATGGATAAGCTCTCTCAT-----CAT 195

Qy 67 ValAspGlnValIleLeuLeuTyrsArgIleAspS-----IleTyrsAspAspTyTyrs 84
 196 ACCGAAAGGGGGTCATCTGCCGTTCAACAAACATCACCTCAGGGTGAGCTTAT 255

Qy 85 GlnAspIleGlyArgValHisPheThrSerAspAspIleGlySerGlyAspAlaser 104
 256 -----AGAATCGCGTCAGCATA---TCCAACATGCGAGCAGTCCGATGCCCTCC 303

Qy 105 IleAsnValThrAsnLeuGlnIleUserAspIleGlyThrTYGlnCysLysValysLys 124
 304 ATCACCATTGATCAGCTGACATGGCTGACAAACGGCACCTAGAGCTGCTGCTG 363

Qy 125 AlaProGlyVal---GlyAspIleS-----IleGlnLeuThrValLeuLeuLysPro 141
 364 ATTCAGACCTGGAGGGCACCAAGTCAGTGICCCCCGTTGCTCTGCGCACCC 423

Qy 142 SerGlyThrArgCysTyrvAlaSpIleGlySerGluGluIleGlyAsnAspPheLysLeuLys 161
 424 TCCAAACCCAGAAATGCCGATCGAGGAGAGACCATTAATGGGAAACATCCAGCTGACC 483

Db 162 CysGluProIleGlyGluGlySerIleProLeuTyrglurGlnIleLeuSer---Asn 180

Qy 484 TGCCAACTCAAAGGAGGCTCACCAACCCCTAGTACAGCTGGAGAGGTACACACATCTG 543

Db 181 SerGlnIleLeuProThrLeuTripleUalaGluMetThrSer---ProValleSerVal 199

Qy 544 AATCAGGGCGAGCC-----CTGCCAACCCAGCTGAGTCAGCTGCCCTCTCCTG 594

Qy 200 LysAsnAlaSerThrGluTyrglyIleThrSerCysThrVallysAsnArgValGly 219
 595 AAGAAATATCTCCACAGACACATCGGGTTACTACATCTGTTACCTCCAGCAATGAGGG 654

Db 220 SerAspGlnCysIleLeuArgIleAspValValProProSerAsnArgGalaGlyThrIle 239

Qy :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||:
 655 AGCGAGTCTGCACATCACGGTGGCCCTCAGATCTCTCCATGAACTGGCTCTGTAT 714

Db 240 AlaGlyIleAlaValIleGlyValLeuAlaValIleValIleGlyLeuIleLepheCys 259
 715 GTGGGCATCGGGTGGGGTGGTGGCAGCCCTCATTCATGCACTCATCTACTGC 774

Qy RESULT 6 US-09-068-051A-23 Sequence 23, Application US/09068051A ;
 Patent No. 6291235 ; GENERAL INFORMATION: ; APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd; Simpson, Richard J.; Nice, Edouard; Moritz, R. L.; Catimel, B.; Ji, Hong; Burgess, Anthony W.;

Length: 960
 Matches: 89
 Conservative: 53
 Mismatches: 96
 Deletions: 23
 Gaps: 11

TITLE OF INVENTION: Colon Cell And Colon Cancer Cell Associated Nucleic Acid Molecules, Protein And Peptides NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: Fulbright & Jaworski LLP STREET: 666 Fifth Avenue CITY: New York City STATE: New York ZIP: 10103 COMPUTER READABLE FORM: MEDIUM TYPE: Disquette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/068-051A FILING DATE: 10-Dec-1998 CLASSIFICATION: 435 PRIORITY APPLICATION DATA: APPLICATION NUMBER: 08/597,495 FILING DATE: 02-Feb-1996 APPLICATION NUMBER: 08/511,876 ATTORNEY/AGENT INFORMATION: NAME: Hanson, No. 6291235 man D. REFERENCE/DOCKET NUMBER: LUD 5316.2 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3168 FAX: (212) 752-5958 INFORMATION FOR SEQ ID NO: 23 REFERENCE/DOCKET NUMBER: LUD 5316.2 SEQUENCE CHARACTERISTICS: LENGTH: 960 nucleotides TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear SBSEQUENCE DESCRIPTION: SEQ ID NO: 23 US-09-068-051A-23 Alignment Scores:

Pred. No.: 3.39e-34 Length: 960
 Score: 351.50 Matches: 89
 Percent Similarity: 54.41% Conservative: 53
 Best Local Similarity: 34.10% Mismatches: 96
 Query Match: 25.86% Deletions: 23
 DB: Gaps: 11

US-09-899-634C-2 (1-261) x US-09-068-051A-23 (1-960)

Qy 10 LeuCysGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluglnMetIle 29
 Db 34 CTCGTGAGTAGGGTGACCGTGCATGCCCTCTGGAACACTCCACCTCCAGT 93

Qy 30 GluLysAlaLysGlyGluThrAlaTyroLeuProCysArgPheThrLeuGlyProGluAsp 49
 94 CGGGCTTGCAGGAAAGAGTGTACCCCTGCCCTGACCTACACTCCACCTCCAGT 153

Qy 50 GlnglyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspIleGlnLys 66
 154 CGAGAGGCACT----ATCAATGGATAAGCTCTCTCAT-----CAT 195

Qy 67 ValAspGlnValIleLeuLeuTyrsArgIleAspS-----IleTyrsAspAspTyTyrs 84
 196 ACCGAAAGGGGGTCATCTGCCGTTCAACAAACATCACCTCAGGTGAGCTTAT 255

Qy 85 GlnAspIleGlyArgValHisPheThrSerAspIleGlyAspAlaser 104
 256 -----AGAATCGCGTCAGCATA---TCCAACATGCTGAGCAGTCGATGCCCTCC 303

Qy 105 IleAsnValThrAsnLeuGlnIleUserAspIleGlyThrTyrsGlnCysLysValysLys 124

SEQUENCE CHARACTERISTICS:
 LENGTH: 2555 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-597-495B-29

Alignment Scores:
 Pred. No.: 1.64e-33
 Score: 351.50
 Percent Similarity: 54.41%
 Best Local Similarity: 34.10%
 Query Match: 25.86%
 DB: 1 Gaps: 11

US-09-899-634C-2 (1-261) x US-08-597-495B-29 (1-2565)

Qy 10 Deucysglyvalalasplauserleuthrthrprogluasnmetile 29
 Db 146 CTCCTGCAGCTGGGTGACCGTCTGGAACACTCCGCGACAGCTT 205
 Qy 30 Gluylsalaysglututrlalatryleuprocyargphehrleuglyproguasp 49
 Db 206 CGGCCTCGGGAAAGAGTGTACCTGACCTGACTCCACTCGT 265
 Qy 50 Glnglyproleusaspileglutp-----leuserasproalaaspasnlyls 66
 Db 266 CGAGAGGACT---ATCAATGGGATAAGCCCTCTCACT-----CAT 307
 Qy 67 Valaspglnvalleuleleutyrserglyasplys-----iletyraspaspvtyr 84
 Db 308 ACGGAAAGGGGGTCACTGGCGGTTCAAACAACATCCATGGTACCTT 367
 Qy 85 Glnaspleuysglvargvalhisphehrserasnpleulysserglyasplaser 104
 Db 368 -----AGAATGCCGAGCATA---TCCAACATGCTGAGTCGCGATGCTCC 415
 Qy 105 Ileasnvalthrasnleuasnleuasnleuasnleuasnleuasnlyls 124
 Db 416 ATCACCATGTCAGTGACCATGGTGAACACGGACCTAACGGACCTTCCTG 475
 Qy 125 AlaProGlyVal--GLYASPLYLYS-----IleGlnleuthvalleuleulysPro 141
 Db 476 ATGTCAGACCTGGGGCAACACCAAGTCAGCAGTCGCGCTGTTGCTGCCCC 535
 Qy 142 SerGlyThraGlyCysTyrValAspGlySerGluGlyIleGlyAspAspHlysLys 161
 Db 536 TCCAAACCAGATGGCGATGAGGAGGACCATTAATGGAACACATCCAGTGACC 595
 Qy 162 CysGluProlysLeuAspLeuAspLeuAspLeuAspLeuAspLeuAspLeuAsp 180
 Db 596 TGCCAACTACAGAGGAGGCTCAGCAACCCCTCACTGAGCTGAGAGGAGG 655
 Qy 181 SerGlylysLeuuprohrleutrpheualgluimetthrser---Provallreserval 199
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 Qy 200 LysAspAlaSerThrGlutyrSerGlyThrTyrSerCysThrVallysAspArgValGly 219
 Db 707 AGAAATATCCTCACAGACATCGGTTACTACATCTGACTCCAGCAATGAGGGG 766
 Qy 220 SerAspGlyCysLeuLeuArgLeuAspLeuAspLeuAspLeuAspLeuAspLeuAsp 239
 Db 767 ACCAGCTCTCACACATCACGGTGGCGCTGAGTCAGCTCCCTCATGAGCTGCGCCCTGTAT 826
 Qy 240 AlaGlyAlaValleuleGlyValleulalalanvalleuleGlyLeuilePheCys 259
 Db 827 GTGGGATCGGGTGGCGTGTGAGCCCTCATTATCATGAGTCATCATATCTACTGC 886
 Qy 260 Cys 260
 Db 887 TGC 889

RESULT 7
 US-08-597-495B-29
 Sequence 29, Application US/08597495B
 GENERAL INFORMATION:
 Patent No. 512369
 APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
 APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
 APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
 APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
 TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/597,495B
 FILING DATE: 02-Feb-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/511,876
 FILING DATE: 04-Aug-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 5712369man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5316.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 29


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242 ATGGAGCCATTCTTACTTCTCAAGGTGGACAGCTGTTAGGCATGGGAAATT 301
Db QY 20 LeuserleRlhThrProgluImmetIleglyLysalysglyLuguthralatyleu 39
QY 97 TRCACGNGCCCCGGGGCCTCACAAATGGAGCGGTAGAGGAGAAGTGGTCTC 156
Db 302 AAAGATCGAACTTACGAGA 340
Db QY 40 ProCysArgPhrThrLeuglyProgluAsp-----GlnGlyProle 53
QY 104 SerileasnValThrAsnLeuglnleuSerAspIleglyThrTyrglnCyslys 123
Db QY 141 ProSerGlyThrArgCysTyryValaspIlySerIleglyAsnAspPhelyleu 160
Db QY 124 LysalaPro-----GlyValglAsnLysIleGlnleuthrValleuLys 140
Db QY 401 AACCCCCAGACTTCTGGCCAAACCAAGGATCTCAAGCTGTCAGTGTTAGGAA 460
Db QY 161 LysCysGluProLyGluGlyserLeuProLeuLeuTygLuTrpGlnLysIleu 180
Db QY 521 TCTGTCTCTCGCGCTTGTAGCAGCCTCCCGTGTACTACGCGATAACTTGAGGA 580
Db QY 461 CCTCTTCAAGCCCTTGTAGCGTCAAGGAGACGAGAACCTGGCCACACTTTCCCT 520
Db QY 181 SerGlnIysLeuprothrLeutpleuIalgluMetThrSerProvalleuVal 200
Db QY 581 AGAGACATCGIGGCCATGTAAGAAACTCAACCCAAACACCGGGATTTGGTCAITGA 640
Db QY 201 AsnAlaserthrIlySerGlyThrThrSerCysThrvalLysAsnArgvalGlySer 220
Db QY 641 RAACTGACAATTGTAAGCAAGTTTACCTGACTGTTACAGTGACTGCTGCACTG 700
Db QY 221 AspGlnCysLeuleuargLeuaspValValProProserAsnArgalaglyThrIleala 240
Db QY 701 AGTTCCTGC-----GAATCGATCTACTCTCTCACATCCAGAACTGGAATCTC 754
Db QY 241 GIYALIValIleGlyValleu--AlaLeuValleuIleGlyLeuIleIlephe 258
Db QY 755 GGGCCTGTAGTGTAGCCTGGTAGTCCGCCATCATCTCTGTGTGCTC 811
Db QY RESULT 13
Db QY US-09-336-536-38
Db QY ; Sequence 38, Application US/09336536
Db QY ; Patent No. 6,406884
Db QY ; GENERAL INFORMATION:
Db QY ; APPLICANT: Leiby, K.
Db QY ; APPLICANT: McKay, C.
Db QY ; APPLICANT: Bosone, S.
Db QY ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
Db QY ; FILE REFERENCE: 7853-14
Db QY ; CURRENT APPLICATION NUMBER: US/09/336, 536
Db QY ; CURRENT FILING DATE: 1999-06-18
Db QY ; NUMBER OF SEQ ID NOS: 75
Db QY ; SOFTWARE: PatentIn Ver. 2.0
Db QY ; SEQ ID NO: 38
Db LENGTH: 1182
Db TYPE: DNA
Db ORGANISM: Mus musculus
Db US-09-336-536-38
Db Alignment Scores:
Db Pred. No.: 5.51e-21
Db Score: 246.50
Db Percent Similarity: 47.46%
Db Best Local Similarity: 28.62%
Db Query Match: 18.14%
Db DB: 4
Db
Db QY RESULT 14
Db QY US-09-336-536-37
Db QY ; Sequence 37, Application US/09336536
Db QY ; Patent No. 6,406884
Db QY ; GENERAL INFORMATION:
Db QY ; APPLICANT: Leiby, K.
Db QY ; APPLICANT: McKay, C.
Db QY ; APPLICANT: Bosone, S.
Db QY ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
Db QY ; FILE REFERENCE: 7853-14
Db QY ; CURRENT APPLICATION NUMBER: US/09/336, 536
Db QY ; CURRENT FILING DATE: 1999-06-18
Db QY ; NUMBER OF SEQ ID NOS: 75
Db QY ; SOFTWARE: PatentIn Ver. 2.0
Db QY ; SEQ ID NO: 37
Db LENGTH: 1846
Db TYPE: DNA
Db ORGANISM: Mus musculus
Db US-09-336-536-37

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Search completed: July 12, 2003, 13:00:48
Job time : 53 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 12:41:12 ; Search time 138 Seconds

(without alignments)
2986.361 Million cell updates/sec

Title: US-09-899-634C-2
Perfect score: 1359

Sequence: 1 MALLFCVLLCGVADLRTSL.....AVIGVLLALVLGLIIFCCR 261

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	Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 1105431 seqb, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-THR=human40_cdi -LIST=200 -THR SCORE=pc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=P2O -NORMEXT -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=@US9899634 @CGN_1_1_125 @runat_09072003_11142_16473
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result % Query Length DB ID Description

Result	Score	Query	Length	DB	ID	Description
1	1359	100.0	4286	10	US-09-899-634A-1	Sequence 1, Appli
2	1353	99.6	1098	3	US-09-899-634A-3	Sequence 3, Appli
3	1238	91.1	2434	10	US-09-971-798-1	Sequence 1, Appli
4	1238	91.1	2473	9	US-10-176-847-77	Sequence 77, Appli

ALIGNMENTS

RESULT 1

US-09-899-634A-1
; Sequence 1, Application US/09899634A

; Patent No. US20020059634A1
; GENERAL INFORMATION:

; APPLICANT: Thomas Buehler, Reto Andreas Gradient, Reinhard Korn, Rao Movva

; TITLE OF INVENTION: pCAR and its uses

; FILE REFERENCE: 4-31499A

; CURRENT APPLICATION NUMBER: US/09/899,634A

; CURRENT FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 1

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: porcine

; FEATURE: CDS

; LOCATION: (3229) . (4014)

US-09-899-634A-1

Alignment scores:

Pred. No.:	8.61e-172	Length:	4286
Score:	1359.00	Matches:	261
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indices:	0
DB:		Gaps:	0

US-09-899-634C-2 (1-261) x US-09-899-634A-1 (1-4286)

Qy 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 3229 ATGGCGCTCCCTGCCTGCTTGCTGCTCCCTGCGGAGTCGGCAATCTAACAGATTG 3288

Qy 21 SerIleThrProGluGlnMetIleGluLysAlaLysGlyGlutnAlaThrLeuPro 40
Db 3289 AGTATCACACTCTGCTGAAGCAGATGATGAAAGGCCAAAGGCCAACTGCTTATTGCA 3348

Qy 41 CYSArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluLeuLeuSer 60
Db 3349 TCGAGATTACCTGGGAGCAGAGACAGGGCCGCTGACATCGAGTGCTGCTGTCA 3408

Qy 61 ProAlaAspGlnIleAsnAlaGlyValAlaAspLeuIleLeuThrSerGlyAspIleThr 80
Db 3409 CCAGCTGATAATCAGAAGTTGAGCTGAGATTTATCTGGAGACAATTAT 3468

Qy 81 AspAspTyTyrgInAspLeuLysGlyValAlaAspLeuIleLeuThrSerGlyAspIleThr 80
Db 3469 GAGCACTACTACCAAGAGCTGAAGGAGCTGACATTTCAAGTAATGATCTCAATCA 3528

Qy 101 GluAspAlaSerIleAsnValIleAsnLeuGlyLeuSerAspIleGlyThrTyrgInCys 120
Db 3529 GGTCATGCACTAAATGAACTCAAGTCAGTTGTCAGATTTGGCACATTCAGTC 3588

Qy 121 LysValIleIleuAlaProGlyValGlyAsnLysIleGlyLeuThrValLeuLeuLys 140
Db 3649 CCTTCAGGTACAAGATGTTATGTTGATGCTAGAGAAATGGAATGATCTAACTA 3708

Qy 161 LysCysGluProLygSglGlyYsRleuProLeuLeuThrGluTrpGlyIleUserAsn 180
Db 3709 AAATGTAACCAAGAGGTCACTCCATTACTATGAAATGGCAGNATGTCAT 3768

Qy 181 SerGlnIleuProThrLeuLeuProLeuAlaGluMetThrSerProValIleLeuLys 200
Db 3769 TCACAGAGCTGCCACCTTGTTGTTAGAGATAATGCTCATGTATCTGAA 3828

Qy 201 AsnAlaSerThrGluTyTyrgInAspCysThrValIleLeuLeuAspIleGlyIle 220
Db 3829 AATGCCCTCATGATGATCTGCGACATACAGCTGACCTGAAACAGAGGGCT 3888

Qy 221 AspGlnCysIleuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLea 240
Db 3889 GATCAGTCCTGCCTGCCTGGATGTTCTCTCAATAGCTGGAGCATCCA 3948

Qy 241 GlyAlaValIleGlyValLeuLeuAlaLeuValIleLeuGlyIleLeuLeuPheCys 260
Db 3949 GGACTCTGTTATAGAGTTTGCTGCTGCTGTCATGTCATCTATCTGTT 4008

Qy 261 ARG 261
Db 4009 CGT 4011

RESULT 2

US-09-899-634A-3
; Sequence 3, Application US/09899634A
; Patent No. US20020059654A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadient, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: pCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09-899, 634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 1098

; TYPE: DNA
; ORGANISM: porcine
; FEATURE: ;
; NAME/KEY: CDS
; LOCATION: (1)..(1098)
; US-09-899-634A-3

Alignment Scores:
Pred. No.: 6.42e-172 Length: 1098
Score: 1353.00 Matches: 259
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.62% Mismatches: 0
Query Match: 99.56% Indexes: 0
DB: 10 Gaps: 0

US-09-899-634C-2 (1-261) x US-09-899-634A-3 (1-1098)

Qy 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 1 ATGGCGCTCCCTGCCTGCTCTGCTCTGCGGAGTCGGCAATCTAACAGATTG 60

Qy 21 SerIleThrProGluGlnMetIleGluLysAlaLysGlyGlutnAlaThrLeuPro 40
Db 61 AGTATCACACTCTGCTGAAGCAGATGATGAAAGGCCAACTGCTTATTGCA 120

Qy 41 CYSArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluLeuLeuThr 80
Db 61 AGTATCACACTCTGCTGAAGCAGATGATGAAAGGCCAACTGCTTATTGCA 120

Qy 81 AspAspTyTyrgInAspLeuLysGlyValAlaAspLeuIleLeuThrSerGlyAspIleThr 80
Db 81 AATGCCCTCATGATGATCTGCTGTTAGAGATAATGCTCATGTCATCTGCTA 360

Qy 101 GluAspAlaSerIleAsnValIleAsnLeuGlyLeuSerAspIleGlyThrTyrgInCys 120
Db 101 AAATGAAAGGCTCTGGCTGAAATGAGCTAACATCTACAGTCATGATCTCAATCA 300

Qy 121 LysValIleIleuAlaProGlyValGlyAsnLysIleGlyLeuThrValLeuLeuLys 140
Db 121 TCGAGATTACCTCTGCTGAGACAGACAGGGCCCTGGACATCGATGCTGCTCA 180

Qy 161 LysCysGluProLygSglGlyYsRleuProLeuLeuThrGluTrpGlyIleUserAsn 180
Db 161 CCAGCTGATAATCAGAGGTGATCAGTGTATTTATCTGGAGACAATTAT 240

Qy 181 SerGlnIleuProThrLeuLeuProLeuAlaGluMetThrSerProValIleLeuLys 200
Db 181 AATGCCCTCATGATGATCTGCTGTTAGAGATAATGCTCATGTCATCTGCTA 360

Qy 201 AsnAlaSerThrGluTyTyrgInAspCysThrValIleLeuLeuAspIleGlyIle 220
Db 201 AAATGAAAGGCTCTGGCTGAAATGAGCTAACATCTACAGTCATGATCTCAATCA 420

Qy 221 AspGlnCysIleuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLea 240
Db 221 AATGCCCTCATGATGATCTGCTGTTAGAGATAATGCTCATGTCATCTGCTA 480

Qy 241 GlyAlaValIleGlyValLeuLeuAlaLeuValIleLeuGlyIleLeuLeuPheCys 260
Db 241 GATCAGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 720

Qy 261 ARG 261
Db 261 TCAAGAGCTGCCACCTGTTGAGCAGAAACAGATGTTCTGTTGAA 600

Qy 4009 CGT 4011

RESULT 3
; Sequence 1, Application US/09971798-1
; Patent No. US20020132769A1

; GENERAL INFORMATION:
; APPLICANT: NO: US20020132769A1artis AG
; TITLE OF INVENTION: Targeting molecules
; FILE REFERENCE: 4-31615/GTI
; CURRENT APPLICATION NUMBER: US/09/971,798
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; LOCATION: (60)..(1157)
; OTHER INFORMATION:
; US-09-971-798-1

Alignment Scores:
; Pred. No.: 6.8e-156
; Score: 1238.00
; Percent Similarity: 94.25%
; Best Local Similarity: 89.27%
; Query Match: 91.10%
; DB: 10 Gaps: 0 ; SEQ ID NO 77 ; LENGTH: 2434

US-09-899-634C-2 (1-261) x US-09-971-798-1 (1-2434)

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; Db 60 ATGGCGCTCCCTGCTTCGTCCTGTGGAGTAGTGATTGCCAGAGTTTG 119

Qy 21 SerIleThrProGluGlnMetIleGluIleAlaValGlyGluThrAlaTyLeuPro 40
; Db 120 AGTATCACTACTCTCTGAAGAGATGATGATGAAAGCCAAAGGGAATGCTATGCCG 179

Qy 41 CysArgPheThrIleGlyProGluAspGlnGlyProteoAspIleGluTrpLeuUser 60
; Db 180 TGCAGATTACGCTAGTCCGGARGAACGGACCGCTGGCATCGAGTGCTGATACTCA 239

Qy 61 ProAlaAspAspGlnIleValAspGlnValIleLeuTerSergIYasIleTer 80
; Db 240 CCAGCTGTATATCAGAAGGGATCAAGTGATTATTATTCGGAGACAATTAT 299

Qy 81 AspAspTYrGlnAspLeuIleGlyArgValHisPheTerSerAsnAspLeuUser 100
; Db 300 GATGACTACTATCCAGATCTGAAGAGCCGAGTACATTACGAGTATGACTCAAATCT 359

Qy 101 GLYAspAlaSerIleAsnValThrAspLeuGlnLeuSerAspIleGlyThrIleGly 120
; Db 360 GGTTGATGATCATATAATGTAAGCACTTGATGAGATATCTACTGTC 419

Qy 121 LysValIlysLysAlaProGlyValGlyAsnIlysLysIleGlnLeuThrValLeuIys 140
; Db 420 AAAGTGAAAAAAGCTCTCTGTGTGCAATTAAGAAGATTCTCTGGTAGTTCTGTGTAAG 479

Qy 141 ProSerGlyLyrThArgCysTyValAspGlySerGluGluIleGlyAsnAspPhenylLeu 160
; Db 480 CCTTCAGGTGGAGATGTTAGCTGATGATGAGCTGAGAAATGAGCTTAAGATA 539

Qy 161 LysCysGluProGlyGluIleSerLeuProLeuTerGluGlnGlyLeuUserAsn 180
; Db 540 AATGTTGACCATAGAGGGTTACTTCATACAGTATGGCAAAATGTGTCGAC 599

Qy 181 SerGlnIlysLeuProThrLeuTopleuAlaGluMetThrSerProValIleSerValIys 200
; Db 600 TCACAGAAAATGCCACTCATGGTTAGCAGAAATGACTTCATCTGTTATCTGTAA 659

Qy 201 AsnAlaSerThrGluTySerGlyThTySerCysThrValIlysAsnArgValGlySer 220
; Db 660 AATGCTCTCTGAGTACTCTGGACATACGGTGACAGTGAGAAACAGCTGGCTCT 719

Qy 221 AspGlnCysLeuLeuArgLeuAspValProProSerAsnArgAlaGlyThrIleAla 240

RESULT 4
; US-10-176-847-77
; Sequence 77, Application US/10176847
; Publication No. US20030068636A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/10/176, 847
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77 ; LENGTH: 2473
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-176-847-77

Alignment Scores:
; Pred. No.: 6.97e-156 Length: 2473
; Score: 1238.00 Matches: 233
; Percent Similarity: 94.25% Conservative: 13
; Best Local Similarity: 89.27% Mismatches: 15
; Query Match: 91.10% Indels: 0
; DB: 9 Gaps: 0 ; SEQ ID NO 77 ; LENGTH: 2473

US-09-899-634C-2 (1-261) x US-10-176-847-77 (1-2473)

Qy 1 MetAlaLeuLeuLeuCysPheValLeuCysGlyValAlaAspLeuThrArgSerLeu 20
; Db 94 ATGGCGCTCCCTGCTTCGTCCTCTGCTCTGCTGGAGTAGTGATTGCCAGAGTTG 153

Qy 21 SerIleThrProGluGlnMetIleGluIleAlaValGlyGluThrAlaTyLeuPro 40
; Db 941 ATGATCACTACTCTGAAGAGATGATGATGAAAGCCAAAGGGAATGCTATGCCG 213

Qy 41 CysArgPheThrIleGlyProGluAspGlnGlyProteoAspIleGluTrpLeuUser 60
; Db 214 TCCAAATTACGCTTAGTCCGGAGAACGGACCGCTGGACATCGAGTGGCTGATATCA 273

Qy 61 ProAlaAspAspGlnIleValAspGlnValIleLeuTerSergIYasIleTer 80
; Db 61 ProAlaAspAspGlnIleValAspGlnValIleLeuTerSergIYasIleTer 80

Qy 81 AspAspTYrGlnAspLeuIleGlyArgValHisPheTerSerAsnAspLeuUser 100
; Db 274 CCAGCTGATATCAGAAGGGATCAAGTGTTATTTATTCGGAGACAATTCT 333

Qy 121 LysValIlysLysAlaProGlyValGlyAsnIlysIleGlnLeuThrValLeuIys 140
; Db 334 GATGACTACTATCCAGATCTGAAGCCGAGTACATTACGAGTATGATCTCAAACT 393

Qy 101 GLYAspAlaSerIleAsnValThrAspLeuGlnLeuSerAspIleGlyThrIleGly 120
; Db 394 GGTGATGTCATCATATAATGTAAGAATTAACGTCAGTATGGCACATATCAGTGC 453

Qy 121 LysValIlysLysAlaProGlyValGlyAsnIlysIleGlnLeuThrValLeuIys 140
; Db 454 AATGTTGAAAGCTCTGGCTTGCAATAGAGTTCATCTGGTAGTTCTGTGTAAG 513

Qy 141 ProSerGlyLyrThArgCysTyValAspGlySerGluGluIleGlyAsnAspPhenylLeu 160
; Db 514 CCTTCAGGTGGAGATGTTAGCTGTTGAGCTGAGAAATGGAGTTGACTTTAGATA 573

QY 161 LysCysGluProLysglygluglySerLeuProLeuLeuTyrglutpGlyLysLeuSerAsn 180
 Db 574 AAATGGAAACCAAAGAGGTCACTTCAATTACAGTAGTGCGAAAATTGTCGTGC 633
 QY 181 SerGlnLysIleuproThrLeuIprLeuAlaGluMetThrSerProValleSerValle 200
 Db 634 TCACAGGAAATGCCACTCTCATGGTACAGTCAGAAATCTCTTATCTGAA 693
 QY 221 ASPGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLea 240
 Db 754 GATCAGGCGCTTGAGTACTCTGGACATACTGAGTCAGTCAGAA 753
 QY 241 GlyAlaValleGlyAlaLeuLeuAlaLeuValleLeuLeuLeuLeuLepheCysCys 260
 Db 814 GGAGCCATTATAGGAATTGCTGCTCTAGGCTTATGGCTTATCTGCTA 873
 RESULT 5 US-09-992-598-504
 Sequence 504, Application US/09992598
 Patent No. US20021603841
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspetter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Andrej
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hiltz, Daniel
 APPLICANT: Kijaviv, Ivar J.
 APPLICANT: Napior, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paon, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C20
 CURRENT APPLICATION NUMBER: US/09/992, 598
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/1049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 9.76e-156 Length: 3060
Score: 0.238.00 Matches: 233
Percent Similarity: 94.25% Conservative: 13
Best Local Similarity: 91.27% Mismatches: 15
Query Match: 91.10% Indels: 0
DB: 9 Gaps: 0

US-09-899-634C-2 (1-261) x US-09-989-293A-504 (1-3060)

QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 77 ATGGCGCTCCGCTGCTGCTGCGACTAGGATTCGCCAGAGTT 136

QY 21 SerIleThrProIluGlnMetIleGluLysAlaLysGlyGluThrAlaTyRleuPro 40

Db 137 AGTATGACTACTCTGAGAGATGATGATGAAAGCCAAGGGAAACTGCCTATGCCA 196
QY 41 CYSArgPheThrLeuGlyProGluAspGlyLysPheLeuAspIleGluTripleutUser 60
Db 197 TCCAAATTAGCTTGCTGCTGGAAAGACGCCGACCATCGAGGTGATATCA 256
QY 61 ProAlaAspAspAnglylvsValAspGinvalleleutyrSerGlyAspSleTyr 80
Db 257 CCAGCTGATAATCAGAGGTGGATCAGTGATTATTATCTGGAGCAAATTAT 316
QY 81 ASPASPYRTGlyAspLeuYsGlyArgValHisPheThrSerAsnAspLeuSer 100
Db 317 GATGACTATCCAGATCTGAAGGCCGAGTACATTAGAGTAATGAACTCAATCT 376
QY 101 GlyAspAlaSerIleLeuValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
Db 377 GGTGATCCTCATATAGTACGAACTGAGTGGCATATCGAGTGGCACATATCGTC 436
QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysLysLeuIleutyrSerGlyAspSleTyr 140
Db 437 AAAGTGAAGAAAGCTCCTGGGTTGCAATAAGATCATCTGGTAGTTCTGTTAG 496
QY 141 ProSerGlyThrArgCystValAspGlySerGlyGluIleGlySerAsnAspPheLysLeu 160
Db 497 CCTCAGGTGGAGATCTTACGTGTTGAGTAACTGAGTCATCTGTTAGTCTGTTAG 556
QY 161 LysCysGlyIleProLysGlySerLeuProIleLeuIleutyrGluTrpGlnLysLeuSerAsn 180
Db 557 AAATGTCACCAAAAGAGGTACTCTTACAGTATGGTGGAAATAATGTCGAC 616
QY 181 SerGlyLysLeuProIleutrpLeuAlaGluMetThrSerProValIleSerValLys 200
Db 617 TCACAGAAATGCCAACCTCTAGTGGTTAGCAGAAATGACTCTCATCTGTTAGAA 676
QY 201 AsnAlaSerThrGlySerGlySerCysThrValLysAsnArgValGlySer 220
Db 677 AATGCCCTCTGAGTACTCTGGACATACAGTGTGACAGAACAGTGGCTCT 736
QY 221 AspGlyCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLeuAla 240
Db 737 GATCAGGCCCTCTGGCTTACAGTGTGCTCTCTCTAACATAAGCTGGACTAATGCA 796
QY 241 GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIlePheCysCys 260
Db 797 GGAGCCCTTATAGGAACCTTCTGCTCTAGGCCTCATTTGCTCATCTTGTCTG 856
QY 261 Arg 261.
Db 857 CGT 859

RESULT 7

US-09-989-735-504 ; Sequence 504, Application US/0999735
; Publication No. US2002019329A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanae, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2730P0C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Lignment Scores:
 Alignment No.: 9.768-156 Length: 3060
 core: 1238.00 Matches: 233
 percent Similarity: 94.25% Conservative: 13
 best Local Similarity: 91.27% Mismatches: 15
 B: Query Match: 91.10% Indels: 0
 Gaps: 9

S-09-899-634C-2 (1-261) x US-09-989-735-504 (1-3060)

1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
 b 77 ATGCGCTCTCTGCTGCTGCTGCGAGACTGGATTGCCAGAGTTC 136

21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyroLeuPro 40
 137 AGTATCACTACTCTGAGAGATGATTGAAAGCCAAAGGGAAACTGCCTATCGCCA 196

41 CYSARGPheThrLeuGlyProGluAspGlyAspGlyProLeuAspIleGluIleLeu 60
 197 TGCACATTTCAGCTTAGTCGGAGAACCCAGGGACGGCTGGACATCGGAGTGCTGATATCA 256

61 ProAlaAspGlyGlnLySValAspGlyValIleLeuTyrIleGlyAspIleTyr 80
 b 257 CCASCTGATAATCAGAAGTGGATCAAGTATTATTTATCATTGGAGCAAAATTAT 316

81 AspAspTyrTyrGlnIleAspLeuLysGlyArgValHisPheThrSerAsnAspLeuSer 100
 317 GATGACTACTATCCAGATCTGAAGGCCGAGTACATTTRAGAGTAATGATCTCAACT 376

101 GlyAspAlaSerIleAsnValThrAsnLeuGlnIleAspAspIleGlyIleTyrGlnCys 120
 377 GGTGATGCACTCAATAGTAAAGCATTACAATGTCAGATATGGCACATACAGTC 436

121 LysValLysLysAlaProGlyIvaGlyAspIleGlnLeuThrValLeuLys 140
 b 437 AAGTGAAGAAAGCTCTGGTGTGCAATAGAAGATCATCTGGTAGTCTGTAG 496

QY 141 ProSerglyThrArgCysTyrValAspGlySerGluGlyIleGlyAsnAspPhylsLeu 1600
 Db 497 CCTCTAGGTCGAGATGTTACGTGATGGATCTGAGAAATGGAGGACTTAAAGATA 5566
 QY 161 LysCysGluProTysGluGlySleuProLeuIleGluTrpGlyIleSleuSerLys 1800
 Db 617 TCAQAGAAATGCCACTCTCATGGAGAAATGACTCATCTGTATATCTGAA 6766
 QY 201 AspAlaSerThrGluTyrSerglyThrTyrSerCysThrValAspAspArgValGlySer 2200
 Db 677 AACCTCTCTGAGTACTCTGGACATACAGCTGAGAACAGAGGGCT 7366
 QY 221 AspGlnCysLeuIearginLeuAspValValProProSerAsnArgGlyThreonala 2400
 Db 737 GATCAGGCTGTCGGCTAAAGTCGTCCTCAATAAAGCTGACTATTC 7966
 QY 241 GlyAlaValIleGlyValLeuAlaLeuValLeuIleGlyLeuIleIlePheCysCys 2600
 Db 797 GGACCCATTATGGAACTTGTCTGCTAGCCTCATGGCTTACATCTTGTCT 8566

QY 261 Arg 857 CGT 859

RESULT 8
 US-09-930-444-504 ; Sequence 504, Application US/0999044
 Publication No. US20020193300A1
 GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hans Peter
 / APPLICANT: Gerritten, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Gołowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Guirney, Autin L.
 / APPLICANT: Klijavin, Ivar J.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Padni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Walanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 CURRENT APPLICATION NUMBER: US/09990444
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065166
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; PRIOR FILING DATE: 1998-07-02
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 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

 Alignment Scores:
 pred. No.: 9 76e-156
 Score: 128.00
 Percent Similarity: 94.25%
 Best local Similarity: 89.27%
 Query Match: 91.10%

 Length: 3060
 Matches: 233
 Conservative: 13
 Mismatches: 15
 Indels: 0
 Gaps: 0

 US-09-899-634C-2 (1-261) x US-09-990-444-504 (1-3060)

 Qy 1 MetAlaLeuIleLeuCysPheValLeuLeuCysGlyAlaAspLeuThrArgSerLeu 20
 Db 77 ATGGCGCTCCGCGTGCAGTCGCTCCGTTGGGAGTAGTGATTTCGCGAGATTTG 136

 Qy 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGlutThrAlaTyLeuPro 40
 Db 137 AGPATCACTACTCTGAAGAGATGATGAAAGCCAAAGGGAAACTGCCATCTCCA 196

 Qy 41 CysArgPheThrLeuGlyProGluAspGlnGlyProteoAspIleGluTrpIleSer 60
 Db 197 TGCATTAATTACGCTTATGGCCGAGCACAGGGACCGCTGGATCGACTGGCTGATCA 256

 Qy 61 ProGlaAspGlnGlyIleValAspGlnValIleIleLeuTerTserGlyAspIleTyr 80
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 Qy 81 AspAspPTYTrGlnAspLeuLysGlyArgValHisPheThrSerAspAspIleLysSer 100
 Db 317 GATGACTACTATCCAGACTGAAGGCGAGTACATTAGCTGAACTGTCAACT 376

 Qy 101 GlyAspAlaSerIleAsnValIleAspIleGlnIleAspAspIleGlyThrTyrGlnCys 120
 Db 377 GGTCATGTCATCAAATAATGTAACTTACAATCTGTCAGATATTGGCACCATCATGTC 436

 Qy 121 LysValLysLysIleProGlyValGlyAsnLysIleGlnIleThrIleLeuLys 140
 Db 437 AAGTGAAAAGACTCCGGTGTGCAAAATAAGAAGATCTCTGGTGTCTGGTAAG 496

 Qy 141 ProSerGlyThrArgCysTrpValAspGlySerGluGluIleGlyAspAspPheLysIle 160
 Db 497 CCTCAGGGCGGAGATGTGATGATCTGAGAAATGATA 556

 Qy 161 LysCysGluProGlyGluIleSerLeuProLeuLeuThrGluTrpGlnLysIleSerAsn 180
 Db 557 AATGTTGAAACGAAAGGGTCACTTCCATACAGATGAGTGGCAAAATGTCGAC 616

 Qy 181 SerGlnLysLeuProThrIleLeuPheLysGluMetThrSerProValIleSerValLys 200
 Db 617 TCACAGAAATGCCACTCATGGTTAGCAAAATGACTCATCTGTTATCTGTAAA 676

 Qy 201 AspAlaSerThrGluTrpSerGlyThrTyrSerCysThrValLysAspArgGlyIleSer 220
 Db 677 AATGCCCTCTGAGTACTCTGGACATACAGCTGACAGTCAGTCAGAACAAGACTGGCT 736

 Qy 221 AspGlnCysAlaLeuIleAspPheValProProSerAspArgAlaGlyThrIleAla 240
 Db 737 GATCAGTGCCCTGTCGCTCTAACAGTGGCTCCCTCAAAAGTGGACTAATGCA 796

 Qy 241 GlyAlaValIleLeuGlyIleValLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleCysCys 260

 Qy 797 GGAGCCATATAGAACTTGTGCTCTAGCGCTCATGGCTTATCATCTTGTGCT 856

RESULT 9

US-10-053-107-9

Sequence 9, Application US/10053107
 Publication No. US200202192752A1
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Ruma, Daniel
 APPLICANT: Watanabe, Colin K.
 TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 FILE REFERENCE: P1033RC1
 CURRENT APPLICATION NUMBER: US/10/053,107
 CURRENT FILING DATE: 2002-01-17
 PRIOR APPLICATION NUMBER: 60/099601
 PRIOR FILING DATE: 1998-09-09
 PRIOR APPLICATION NUMBER: 60/107783
 PRIOR FILING DATE: 1998-11-10
 PRIOR APPLICATION NUMBER: 60/108802
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 PRIOR APPLICATION NUMBER: 60/112996
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 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: PCT/US01/17800
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: PCT/US01/19692
 PRIOR FILING DATE: 2001-06-20
 PRIOR APPLICATION NUMBER: PCT/US01/21066
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: PCT/US01/21735
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 14
 SEQ ID NO 9
 LENGTH: 3060

; TYPE: DNA		Publication No. US20020197674A1	
; ORGANISM: Homo Sapien		GENERAL INFORMATION:	
Pred. No.:	9.76e-156	Length:	3050
Score:	1238.00	Matches:	233
Percent Similarity:	94.25%	Conservative:	13
Best Local Similarity:	89.27%	Mismatches:	15
Query Match:	91.10%	Indels:	0
DB:		Gaps:	9
US-09-899-634C-2 (1-261) x US-10-053-107-9 (1-3060)			
Qy	1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerIeu	20	APPLICANT: Ashkenazi, Avi J.
Db	77 ATGGCGCCCTCGCTTGCTTCGCTCCCTGCGAGTAGTGGATTGCCAGAGTTG	136	APPLICANT: Baker, Kevin P.
Qy	21 SerIleThrProGluLmMetIleGluLysAlaLysGlyGluThrAlaTyLeuPro	40	APPLICANT: Boosten, David
Db	137 ASTPATCACTCTGAAGAGATGTGAAAGCCAGGGCTGGACATCGAGTGCTGATATCA	196	APPLICANT: Eaton, Dan L.
Qy	41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuLeuSer	60	APPLICANT: Ferrara, Napoleon
Db	197 TGCATTACGCTAGTCCGAGAACGCCAGGGCTGGACATCGAGTGCTGATATCA	256	APPLICANT: Fong, Sherman
Qy	61 ProAlaAspAspGlnLysValAspGlnValLeuIleLeuTySerGlyAspLysIleTyr	80	APPLICANT: Geber, Hans Peter
Db	257 CCAGCTGATAATCAGAACGTTGGAACTAGTGGATTATTATATCTGGAGACAATTAT	316	APPLICANT: Deenoyers, Luc
Qy	81 AspAspTYrgIleAspIleLysGlyArgValHisPheThrSerAsnAspIleUsser	100	APPLICANT: Gerritsen, Mary E.
Db	317 GATGACTTAATCCAGACTGAAAGCCAGCATCGCTGAGTAACTTACAGGTAATGATCTCAACT	376	APPLICANT: Goddard, Andrew
Qy	101 GLYAspAlaSerIleAsnValThrAspIleGluLeuSerAspIleGlyThrTYrgInCys	120	APPLICANT: Grimaldi, J. Christopher
Db	377 GGTGATGGATCAATAATGTAAGCATACAGTGGACATACAGTCAGTC	436	APPLICANT: Gurney, Austin L.
Qy	121 LysValLysLysAlaProGlyValGlyAsnLysIleGlnLeuThrValLeuIys	140	APPLICANT: KjJavin, Ivar J.
Db	437 AAAGTGAAGAAAGCTCCCTGGTGTCAAATAAGAAGATTCATCTGGTACTCTGTTAG	496	APPLICANT: Napier, Mary A.
Qy	141 ProSerGlyThrArgCYS-TyRValAspGlySerGluGluIleGlyAsnAspPhyLysIeu	160	APPLICANT: Onori, Nicholas F.
Db	497 CCTCAGTTGGAGATGTAGTGTGATCTGAGAATCTGAGAAATTGGAACTTAAGATA	556	APPLICANT: Roy, Margaret Ann
Qy	161 LysCysGluProLysGluGlySerIleProLeuTyRglutPheGlyIleLeuSerAsn	180	APPLICANT: Stewart, Timothy A.
Db	557 AACATGTAACCAAAAGAAAGTTTACCTCCATTAGATGATGAGGCTGGCAAAATGCTGAC	616	APPLICANT: Tunas, Daniel
Qy	181 SerGlnGlyLeuProThrLeuIlePheAlaGluMetThrSerProValIleSerValLys	200	APPLICANT: Watanabe, Colin K.
Db	617 TCACAGAAATGCCCCACTTCATGGTTAGCGAGAAATGACTTCATGTTATCTGTTAAA	676	APPLICANT: Williams, P. Mickey
Qy	201 AspAlaSerThrGluItySerGlyThrTySerCysIthValLeuAsnArgValGlySer	220	APPLICANT: Wood, William I.
Db	677 AATGCCCTCTGAGTACTCTGGACATACAGCTGAGTCAGTCAGAACAGAGCTGCCT	736	APPLICANT: Zhang, Zemin
Qy	221 AspGlnCysLeuIleArgLeuAspValProValProProSerAsnArgAlaGlyThrIleIea	240	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Db	737 GATCAGTGCTGCTGCTGCTAACTGTCGCTCCCTCAATAGCTGAGCTAACTGCA	796	Acids Encoding the Same
Qy	241 GlyAlaValLeuGlyValLeuLeuAlaLeuValLeuIleGlyLeuIlePheCysCys	260	FILE REFERENCE: P2770P1C69
Db	797 GGAGCATTATAGGAACTTGTGCTCTGCTCATTTGCTTATCATCTTGTCT	856	CURRENT APPLICATION NUMBER: US/09/989, 730
Qy	261 Arg 261		CURRENT FILING DATE: 2001-11-20
Db	857 CGT 859		PRIOR APPLICATION NUMBER: 60/049787
RESULT 10			PRIOR FILING DATE: 1997-06-16
; Sequence 504, Application US/09989730			PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17			PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12			PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/065311			PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24			PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945			PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25			PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910			PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20			PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322			PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28			PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600			PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07			PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106			PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28			PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607			PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02			PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088609			PRIOR APPLICATION NUMBER: 60/088609
; PRIOR FILING DATE: 1998-06-02			PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759			PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02			PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088026			PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04			PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030			PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04			PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033			PRIOR FILING DATE: 1998-06-04
; PRIOR FILING DATE: 1998-06-04			PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/089554
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/089947
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PRIOR APPLICATION NUMBER: 60/089948
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429

Assignment Scores:	
Pred. No.:	9.76e-156
Score:	1238.00
Percent Similarity:	94.25%
Best Local Similarity:	89.27%
Query Match:	91.10%
BR:	9
Length:	3060
Matches:	233
Conservative:	13
Mismatches:	15
Indels:	0
Gaps:	0

US-09-899-634C-2 (1-261) x US-09-989-730-504 (1-3060)

QY
1 MetAlaLeuIeuLeuCysPheValLeuLeuCysGlyVal

Db
77 ATGGCGCTCCTGCTGCTTGTGCTCTTGCGGAGTAGTGGATTGCCAGAAGTTG 136

QY
21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyrLeuPro 40

Db 137 ÄGTATCACTACTCCTGAAGAGATGATTGAAAAGCCAAAGGGAACTGCCTATCTGCCA 196

PARTY NAME: APPLICANT: Wood, William P. Mickey
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transferred Reference Encoding
FILE REFERENCE: P2130PIC14
CURRENT APPLICATION NUMBER: US/09/99999
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-02 ; PRIOR APPLICATION NUMBER: 60/091978
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PRIOR FILING DATE: 1998-07-07 ; PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09 ; PRIOR APPLICATION NUMBER: 60/092182

Alignment Scores:
Pred. No.: 9.76e-156 Length: 3060
Score: 1238.00 Matches: 233
Percent Similarity: 94.25% Conservative: 13
Best Local Similarity: 89.27% Mismatches: 15
Query Match: 91.10% Indels: 0
DB: Gaps: 0

US-09-899-634C-2 (1-261) x US-09-990-436-504 (1-3060)

QY	1 MetAlaLeuLeuLeuCysPheValLeuCysGlyValAlaAspLeuThrArgSerLeu	20
Db	77 ATGactCTCTGCCTGCTTGCTCGTCTCTGCGGGTAGTGGATTGCCAGAGTTG	136
QY	21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyrIeuPro	40
Db	137 AGTATCACTACTCTGAAGAGATGATGAAACCAAAGGGAACTGCCTATCTGCCA	196
QY	41 CysArgPheThrLeuGlyProGluAspGlyProLeuAspIlePheLeuUserSer	60
Db	197 TGCAAAATTAGCTGTAGTCGCCGAGACCGGGACGCTGACATGAGTGCTGATCA	256
QY	61 ProAlaAspAsnGlnLysValAspGlnValLeuIleLeuTyrSerGlyAspLysTleYr	80
Db	257 CCAGCTGATATCAAGAGGGATGACGATGATTTATCTGAGACAATTAT	316
QY	81 AspAspTYrGlyGlnAspLeuGlyIArgValHisPheThrSerAsnAspLeuYss	100
Db	317 GATACTACTATCAAGATCTGAAGGCCGAGTACATTTCAGCATATGATGATCTCAAACT	376
QY	101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuAspLeuAspIleGlyThrArgCys	120
Db	377 GGATGTGATGCAATTAATGAACTAACGATTAACGTCAGATATGGCACATATGTC	436
QY	121 LysValLysIleAlaProGlyValGlyAsnLysIleGlnLeuThrValLeuIleLys	140
Db	437 AAGGAAAGAAAGCCTGCTGTCGAATTAAGAGATGATCCTGGTAGTCCTGTAAG	496
QY	141 ProSerGlyThrGlyCysTyrValAspGlySerGluGluIleGlyAsnAspPhenylsLeu	160
Db	497 CCTGAGGTCGAGATGTTAGTGTAGGATCTGAGAATTGGAGTGAATGAGTCAAGATA	556

PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
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 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17

161 LysCysGluProLysGluGlySerIleProLeuIleGluTrpGluTrpGlnIleAsn 180
 557 AAATGTGAACTAACAGAGGTTCACTTACAGTAGTGCGAAATTGTCGAC 616
 181 SerGlyLysLeuProThrLeuTripleuLagLumeThrSerProValIleSerValLys 200
 677 AATGCCCTCTCTGAGTACTCTGGACATACAGCTGACAGAACAAGTGCCCT 736
 617 TCAAGAAATGCCACTTCAGTGTAGCAGAAATGACTTCACTGTATACTGAAA 676
 221 AspGlnCysLeuIleuAgleuaspValValProProSerAspArgAlaGlyThrLeAla 240
 737 GATCAGTCGCTGTTGGCTCTAACGTTGTCCTCCCTCAATTAACGCTGAACT 856
 241 GlyAlaValIleGlyValLeuIaLeuValLeuIleGlyLeuIlePheCysCys 260
 797 GGACCATATTAGGAATTGCTTGTCTAGGCTCATGGCTTATGCTTATCTGT 856
 QY 261 Arg 261
 Db 857 CGT 859

RESULT 12

US-09-991-181-504

Sequence 504, Application US/09991181

Publication No. US20020197615A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William T.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secretin and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730PIC53

CURRENT APPLICATION NUMBER: US/09-991, 181

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

RESULT 13
 US-09-993-687-504
 Sequence 504, Application US/09993687
 Publication No. US20020198149A1

GENERAL INFORMATION:

APPLICANT: Astkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritten, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Hurney, Austin L.
 APPLICANT: Kijaviv, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zemlin, Zheng

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2710PC11

CURRENT APPLICATION NUMBER: US/09/993,687

CURRENT FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

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PRIOR APPLICATION NUMBER: 60/087827

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PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/0889548

PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
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PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090695
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR APPLICATION NUMBER: 60/090699
PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 9.76e-156 Length: 3060
Score: 1238.00 Matches: 233
Score: 94.25% Conservative: 13
Best Local Similarity: 89.27% Mismatches: 15
Query Match: 91.10% Indels: 0
Db: 9 Gaps: 0

US-09-899-634C-2 (1-261) x US-09-993-687-504 (1-3060)

Qy 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspIleThrArgSerIle 20
Db 77 ArgGCCTCCGCTGGTGGCTCTGGCGGAGTAGTGATTGGCATTCGGCTCAAGAATG 136
Qy 21 SerIleThrThrProIleGluLysAlaIysGlyGluThrAlaItyLysPro 40

Db 137 AGTATCCTACTCTGAGAGTGATTGAAGAACGCCAAAGGGAAACTGCCATATGCCA 196
Qy 41 CysArgPheThrLeuGlyProGluArgPheGlyProLeuAspIleGluThrLeuSer 60
Db 257 CGCAAAATTAGCTTAAGCTCCGAGACGAGGACCGCTGGACATCGGGTGTGATCA 256
Db 61 ProAlaAspAlaGlnLysValAspGlnValLeuIleLeuTyrsArgIleTyrs 80
Db 257 AAAGCTGATAATCAGAGGTGGATCAGTGTTATTATTCGGAGACAATTAT 316
Db 81 ASPASPYTrGlnIleLeuGlyArgValIHSpheThrSerIasnAspLeuLysSer 100
Db 317 GATGACTACTATCCAGTCAGTCAGTGAAGGCCGAGTACATTAGAGTATGATCTCAATCT 376
Db 101 GIVASpalaSerIleLeuValThrAspIleGlySerAspIleGlyThrTyrGlyCys 120
Db 377 GETGATCOTCATATATAGTACGAAATTACACTGTCAGTATGGCAGTCATGTG 436
Qy 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys 140
Db 437 AAAGTGAAGAAAGCTCTGGTTGCAATAAGAAGATCATCTGAGTCTGTTGTAAG 496
Db 141 ProSerGlyThrArgCysTyrValArgGlySerGluGluIleGlyAsnAspPhelysLeu 160
Db 497 CCTCAGGTCGAGAGTGTACGTGATGGATCTGAAGAAATTGGAGCTTAAGATA 556
Qy 161 LysCysGluProLygGlySerIleLeuProLeuLeuTyrgIutrgInlyveLeuUserAsn 180
Db 557 AATATGTCGACCAAAGAGGTTCACTTCATACAGTATGAGTGTGGCAAAATGTCG 616
Qy 181 SerGlyNlysLeuProThrLeuIleTriPheAlaGluMetThrSerProValIleSerVal 200
Db 617 TCACAGAAATGCCACTTCAGGTTAGCAGAAATGACTTCATCTGTTGTAAG 676
Db 201 AspAlaSerThrGluTyrsSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
Db 677 AATGCCCTCTGAGACTCTGGACATACCTGTCAGTCAGACAAACAGTGCGCTCT 736
Db 221 AspGlyCysLeuIeuaugLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 737 GATCAGGCCCTCTGGCTCTAACGTTGTCCTCTAACTAAGTGGACTAAATGCA 796
Qy 241 GlyAlaValIleGlyValLeuLeuAlaLeuLeuLeuIleLeuIleLepheCysCys 260
Db 797 GGAGCCATTAGGAACCTTGCTCTAGGCTCTAGGCTCATGGCTTATCATCTTGTG 856
Qy 261 Arg 261
Db 857 CGT 859

RESULT 14

US-09-989-734-504 ; Sequence 504, Application US/09989734
; Publication No. US2003003531A1
; GENERAL INFORMATION:
; APPLICANT: Nahkemazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Sequences Encoding the Same

FILE REFERENCE: P27301C64

CURRENT APPLICATION NUMBER: US/09/989,734

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

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PRIOR APPLICATION NUMBER: 60/088021

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PRIOR APPLICATION NUMBER: 60/090694
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Recd. No.:	9.76e-156	Length:	3060
Score:	1238.00	Matches:	233
Percent Similarity:	94.25%	Conservative:	13
Local Similarity:	91.10%	Mismatches:	15
Query Match:	9	Indels:	0
		Gaps:	0

S-09-899-634C-2 (1-261) x US-09-989-734-504 (1-3660)

QY

Db 181 SerGlnLysLeuProThrIleutPheAlaGluMetThrSerProValLeuSerValYs 200
Db 617 TCACTGAAATGCCCACTTCATGGTAGCGAAATGACTTCATCTTGTAAA 676
Db 201 AspIlaSerThrGluTyrosylIhrTyrosylSerCysThrVallyAsnArgValGlySer 220
Db 677 ATTCGCTCTCTGACTACTTGGAACATACTCCATTACGTGATGTTGCGAACAAATTGTCTGAC 616
Db 221 AspGlnCysLeuLeuLargIleuAspValValProProSerIasnArgAlaGlyThrIleAla 240
Db 737 GATGAGTGCCTGTTGGCTAAAGCTGTGCTTCCTCAAATTAAGCTGGCTTAATGCA 796
QY 241 GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIlePheCysCys 260
Db 797 GGAGCCATTAATGGAACTTGCTCTCTAGGCTCATGGCTCATCTTGTGT 856
QY 261 Arg 261
Db 857 CGT 859

RESULT 15
US-09-937-653-504
; Sequence 504, Application US/09997653
; Publication No. US2003008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashekenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borsstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geurtsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjavin, Ivar J.
; APPLICANT: Nipper, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tomas, Daniel
; APPLICANT: Watanabe, Colm K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PC13B
; CURRENT APPLICATION NUMBER: US/091997-653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

QY

Db 497 CCTTAGGGCCGAGATGTTACGTGATGGATCTGAGAAATTGGAGTTGATA 556
Db 161 LysCysGluProLysGluGlyserLeuProLeuLeuTyrglutpGlnLysLeuSerAsn 180
Db 557 AAATGTGAAACAAAGAGAGTTACTCCATTACGTGATGTTGCGAACAAATTGTCTGAC 616
QY 181 SerGlnLysLeuProThrIleutPheAlaGluMetThrSerProValLeuSerValYs 200
Db 617 TCACTGAAATGCCCACTTCATGGTAGCGAAATGACTTCATCTTGTAAA 676
Db 201 AspIlaSerThrGluTyrosylIhrTyrosylSerCysThrVallyAsnArgValGlySer 220
Db 677 ATTCGCTCTCTGACTACTTGGAACATACTCCATTACGTGATGTTGCGAACAAATTGTCTGAC 616
Db 221 AspGlnCysLeuLeuLargIleuAspValValProProSerIasnArgAlaGlyThrIleAla 240
Db 737 GATGAGTGCCTGTTGGCTAAAGCTGTGCTTCCTCAAATTAAGCTGGCTTAATGCA 796
QY 241 GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIlePheCysCys 260
Db 797 GGAGCCATTAATGGAACTTGCTCTCTAGGCTCATGGCTCATCTTGTGT 856
QY 261 Arg 261
Db 857 CGT 859

OY	261	Arg	261
Db			
	857	CGT	859

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Run on: July 12, 2003, 11:49:47 ; search time 1102 Seconds
 (without alignments)
 3835.773 Million cell updates/sec

Title: US-09-899-634C-2
 Perfect score: 1359
 Sequence: 1 MALLCFLVLLCGVADLITRSI.....AVIGVILALVLVLIGLIIFCCR 261

Scoring table: BIOSUM62

Xgapop 10.0 , Xgapext 0.5

Xgapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delexxt 7.0

Searched:

16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODELL:frame+P2n,model -DEV=xlh
 -Q=/USP2N.spool/US09899634/runat_09072003_111139_16356/app_query.fasta_1.455
 -DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=BITS -START=1 -END=-1 -MATRIX=BIOSUM62 -TRANS=Human40_cdi -LIST=45
 -OUTFILE=EST -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09899634 @CGN 1 1 1456 @runat 09072003_111139_16356 -ICPU=3
 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREBADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

Database :

EST:*

1: em_estba:*

2: em_estbhum:*

3: em_estini:*

4: em_estm1:*

5: em_estov:*

6: em_estpi:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est1:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

RESULT 1
 AL521066
 LOCUS AL521066 LTI_NSL004_NBC2 Homo sapiens mRNA linear EST 13-FEB-2001
 DEFINITION AL521066 LTI_NSL004_NBC2 Homo sapiens mRNA clone CSODB001YD23 5
 PRIMERY
 ACCESSION AL521066
 VERSION AL521066.1 GI:12784559
 KEYWORDS EST.

SOURCE
 human

ORGANISM
 Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 917)
 Li,W., Gruber,C., Jesse,J. and Polaves,D.

AUTHORS
 Full-length cDNA libraries and normalization

JOURNAL		COMMENT	
Unpublished (2001)		Contact: Genoscope	
Genoscope - Centre National de Sequençage		BP 191 91060 Evry cedex - France	
Email: sequefragenoscope.cns.fr, web : www.genoscope.cns.fr.		location/qualifiers	
FEATURES	source		
		1. .917 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DB01Y23" /clone_lib="LTI-NFL004_NBC2" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="DHL0B" /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"	
BASE COUNT	272 a 188 c 218 g 238 t	2 others	
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VERSION	AK004908.1	GI:12836447	
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SOURCE	Mus musculus (strain:C57BL/6J) adult male liver mRNA, clone lib:RIKEN full-length enriched mouse cDNA library		
Locus			
DEFINITION	AK004908		
ORGANISM	Mus musculus	adult male liver mRNA, RIKEN full-length enriched library, clone:1300005A16:coxsackievirus and adenovirus receptor, full insert sequence.	
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	9927953		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	1049374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Isobe, Y., Nakamura, S., Hizama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, S., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequencing analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Akizawa, T., Izawa, M., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, R., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kohchiwa, H., Quackenbush, J., Schriml, L.M., Sasaki, F., Suzuki, R., Tomita, M., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Watanabe, T.,		

TITLE		Functional annotation of a full-length mouse cDNA collection	
JOURNAL		Nature	
MEDLINE		2409 (6821), 685-690 (2001)	
REFERENCE	AUTHORS	polyA_signal	polyA_site
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,			
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Hume,D., Imori,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,			
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,			
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,			
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Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,			
Schröml,L., Shiba,T., Shibata,Y., Shinagawa,A., Shiraki,T.,			
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,			
Tanaka,T., Tezima,Y., Toya,T., Yamamura,T., Yamamoto,I.,			
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and			
Hayashizaki,Y.			
Direct Submission			
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of			
Physical and Chemical Research (RIKEN), Laboratory for Genome			
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),			
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,			
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,			
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,			
Fax: 81-45-503-9216			
Please visit our web site (http://genome.gsc.riken.go.jp/) for			
further details.			
cDNA library was prepared and sequenced in Mouse Genome			
Encyclopedia Project of Genome Exploration Research Group in Riken			
Genomic Sciences Center and Genome Science Laboratory in RIKEN.			
Division of Experimental Animal Research in Riken contributed to			
prepare mouse tissues. First strand cDNA was primed with a primer			
[5'- GAGAGAGAGCGCCGAACTCGACTGTTTGTGTTTGN 3'] cDNA was			
prepared by using trehalose thermo-activated reverse transcriptase			
and subsequently enriched for full-length by cap-trapper. Second			
strand cDNA was prepared with the primer adapter of sequence [5'			
GAGAGAGAGATCCACAGCAGTCATAATTAACTAACCCCCCCC 3']. cDNA was			
cleaved with XbaI and SstI. Cloning sites, 5' end: SstI, 3' end:			
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Qy	201	AsnAlaSerThrGlyLysSerGlyThrTyroSerCysThrValLeuAsnAspGlySer	220
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Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"	Db			
Query Match:	DB:	13		
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82	AspTyrTyrClnAspLeuGly-ProGlnValIleLeuThrSerGlyAspIleuSerPro	81	QY
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VERSION	AU131437.1	GI:10991791	
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BIOCARBATA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	(bases 1 to 879)	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.	
AUTHORS	HRI human cDNA project		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Takeo Isogai		
Genomics Laboratory			
Helix Research Institute			
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan			
Tel: 81-438-52-3975			
Fax: 81-438-52-3975			
Email: genomics@hri.co.jp			
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QY	201	AsnAlaSerThrGlyIleGlySerCysThrValAsnArgAlaGlySer	220
Db	688	ATGGCCCTCTGAGTACTCTGGACATACAGCTGACAGACAGCTGCT	747
QY	221	AspGlyCysLeuLeuArgLeuAspValPro-ProSerAsnArgAlaGlyThrIleAl	240

/lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: pcMVSORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dt) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pcMVSORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :
<http://fulllength.invitrogen.com>"
<http://fulllength.invitrogen.com>"

BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.66e-110 Length: 824
 Score: 1060.00 Matches: 200
 Percent Similarity: 93.39% Conservative: 12
 Best Local Similarity: 88.11% Mismatches: 15
 Query Match: 78.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-899-634c-2 (1-261) x AL534436 (1-824)
 Qy 32 AlanylGlyGluThrAlaTyrLeuProCysArgPheSerGlyProGlnAspGlnGly 51
 Db 1 GCAAAAGGCCAACCTGCCTACTSCATGCAATTACGCTTAGGCCGAGACCGGA 60
 Qy 52 ProLeuAspIleGluTrpLeuSerProAlaAspAspGlnLysValAspGlnValle 71
 Db 61 CGCTGGACCTGAGGGCCGATATCACCGCTGATAATCAGAGGGTGTCAAGTGATT 120
 Qy 72 IleLeuTyrSerGlyAspIleSerTyrAspAspTyrTyrGlnAspLeuLysGlyArgVal 91
 Db 121 ATTATATTCCTGGAGCACAAATTATGAGTACTATCAGATCTGAGAAGCCGAGATA 180
 Qy 92 HisPheThrSerAspAspIleSerGlyAspAlaSerIleAsnValThrAspLeuGln 111
 Db 181 CATTAGAGTAATGATCTCAATCTGGATGCTCAATAAATGTAAGGAAATTACAA 240
 Qy 112 LeuSerAspIleGlyThrTyrGlnLysLysValLysLysAlaProGlyValGlyAsnLys 131
 Db 241 CTGTCAGATATGGCACATATCAGTCGAAGTGAAGTGAAGAAAGCTCCUGGTGTGCAATAAG 300
 Qy 132 LysIleGlnIleThrValLeuLeuIysProSerGlyThrArgCysTyrValAspGlySer 151
 Db 301 AGATTCATCTGGTAGCTCTGTTAAGCCTCAGGTCGAGATGTTAGCTGATGGCT 360
 Qy 152 GluGluIleGlyAspAspPheIleLysCysGluProIysGluGlySerLeuProLeu 171
 Db 361 GAAGAAATTGGAAAGTGACTTAAAGTGAACCAAAGAAGGTTCACCTCCATTA 420
 Qy 172 LeuTyrGluTrpGlnLysLeuSerGlnLysLeuProThrLeuTyrPheLeuAlaGlu 191
 Db 421 CAGTATGAGTGGCAAATATGCTGACTCAGCAGAAATGCCACTCATGGTACAGAA 480
 Qy 192 MetThrSerProValIleSerValLeuAspAlaSerThrGluTyrSerGlyThrTyrSer 211
 Db 481 ATGACTCATCTGTATATCTGTAATAAATATGCCCTCTGACTCTGGACATACAGC 540
 Qy 232 ProSerAsnArgGlyThrIleAlaGlyAlaValLeuIleGlyValLeuAlaLeu 251
 Db 601 CCTTCATAAAAGCTGACTATTGGAGGCCATTATAGCAACTTGCTCTAGCC 660
 Qy 252 LeuIleGlyIleLeuIleLeu 258
 Db 661 CTCATTKGTCTTATCATCTT 681

BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 9.13e-109 Length: 775
 Score: 1049.00 Matches: 205
 Percent Similarity: 92.83% Conservative: 15
 Best Local Similarity: 86.50% Mismatches: 15
 Query Match: 77.19% Indels: 3
 DB: 13 Gaps: 0
 US-09-899-634c-2 (1-261) x BI687131 (1-775)
 Qy 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerIeu 20
 Db 70 ATGCCGCCCTACTCTGCTGCTCTGTCGCGGATTACCGAGTGGTT 129
 Qy 21 SerIleThrThrProGluGlnMetIleGluLysAlaGlyGlyLysGlyAlaTyrLeu 40
 Db 130 AGCATCACTACACCCGAAAGAGATCGAAAAGCCAAAGGGAACATCGGTATCTACCA 189
 Qy 41 CysArgPheThrIleGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuSer 60
 Db 190 TCAAGATTACTCTGACGCCGAGACCA-GGACCACTGAGCATTTGATGGCTGATATCC 248
 Qy 61 ProIleAspAspGlnLysIleAlaPheValLeuIleLeuIty-SerGlyAspIleTyr 80
 Db 249 CGCTCTGATACCATGAGTAGTGGATCAAGTGTATTTGAGACATTTGAGACATTT 308
 Qy 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAspLeuIys 100
 Db 309 GATAACTATCCGGATCTGAAAGGACGGTACATTACAGGATACCGATGTCAGTC 368

Qy 101 GluAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnGly 120
 Db 369 GGGCAGGCATCTATAAATGTCACCAACTTGACACTGCGACATTGCGACTAACAGAGC 428
 Qy 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
 Db 429 AACGTGAAGAACGCCCTGGGTGCCAAATAGAAATTCTGCTGACGGTCTGTGTRAG 488
 Qy 141 ProSerGlyThrArgCysThrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
 Db 489 CCTTCAGGGCACAGATGCTTGAGTGCATCCACTACAGTTGAACTGGCGAACATGTCGAC 548
 Qy 161 LysCysGluProGlySerIleProLeuLeuThrGluTrpGlnLysLeuSerAsn 180
 Db 549 AAATGTGAACTCAAGGAAGGTCCTCCACTACAGTTGAACTGGCGAACATGTCGAC 608
 Qy 181 SerGlnLysIleProThrLeuTriPheLeuAla-GluMetThrSer-ProValLeuSerVal 200
 Db 609 TCCGAGACATGGCTACGCCATGGCGAACATGACGTGACAGGATTCGAAGTCAACCTA 548
 Qy 200 SASnAlaser-ThrGluTyrsThrGlySerCysThrValLeuLysAsnArgValGlyS 220
 Db 669 GAGGCCAGTTGAGTCTGGACATACAGCTGCTGACGGTCAAAACAGAGTAGTCGCT 728
 Qy 220 eraspGlyCysLsLeuLysLeuLysLeuAspValValProProSerAsnArg 235
 Db 729 CTGACCACTGTATGCTGCGACTAGACGTTGCCACCTCCACCGA 775
 RESULT 10
 BI080376 BI080376 779 bp mRNA linear EST 20-JUN-2001
 DEFINITION LOCUS 602876828FL NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008543 5',
 ACCESSION mRNA sequence.
 VERSION BI080376.1 GI:14498706
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammary; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE NIH-MGC http://mgc.ncbi.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNLW1103 row: 9 column: 08
 High quality sequence stop: 767.
 FEATURES source
 1. -779
 /organism="Mus musculus"
 /strain="FVB/N-3"
 /db_xref="Taxon:10090"
 /clone="IMAGE:5008543"
 /clone_libs="NCI_CGAP Mam2"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="DHL0B"
 /notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
 Site 2: NotI; Cloned unidirectionally; Primer: Oligo dT;
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT 212 a 196 c 195 g 176 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2.39e-105 length: 779
 Score: 1019.00 matches: 202
 Percent Similarity: 92.02% Conservative: 17
 Best Local Similarity: 84.87% Mismatches: 14
 Query Match: 74.98% Indels: 5
 DB: 13 Gaps: 0

US-09-899-634C-2 (1-261) x BI080376 (1-779)

Qy 1 MetAlaIleLeuCysPheValLeuLeuCysGlyValAlaAspIleThrArgSerLeu 20
 Db 74 ATGGCGGCCCTACTGCGCTCTGCGGATTCACCGTGGTTG 133
 Qy 21 SerIleIleThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaIleLeuPro 40
 Db 134 AGCATCACTACACCGAACAGAGGATGAAAGGGAAACTGCGTATCACCA 193
 Qy 41 CysArgGlyGluIleGlyProGluAspGlyGlyProLeuAspIleGluTrpLeuSer 60
 Db 194 TSCAAGTTTACTCTACGCTCCGAGACAGGACACTGGACATTGATGGCTGATATCC 253
 Qy 61 ProAlaAspAspGlnLysValAspGlnValAlleLeuThrSerGlyAspIleTyr 80
 Db 254 CGCTCTATAACAGATAGTGGATCAGTGACATTGATGATCTGAGCTA 313
 Qy 81 ASPAspThrTyrGlnAspIleGlyArgValHisIleThrSerAsnAspLeuLysSer 100
 Db 314 GATACTACTATCCGGACTGTAAGAGGGTACATTACAGTAAGATGTCACGCT 373
 Qy 101 GluAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnGly 120
 Db 374 GGCGACCACATCTATAATGTGACCAACTGCGACATGCGACATTGCACTTACAGTC 433
 Qy 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGln-LeuThrValLeuLeu 140
 Db 434 AAATGAGAAAGCCCCTGGCTTGCAAAATCGAAATTCCGGCTCTGCGCTCTGTA 493
 Qy 140 sProSerGlyThrArgCysThrValAspGlySerGluGluIleGlyAsnAspPheLys 160
 Db 494 GCCTTCAGGTACAGATGCTTGCTGGATGGATCGGAACTGCAAGTCAAC 553
 Qy 160 eulysCysGluProGlySerIleProLeuLeuThrGluTrpGlnLysLeuSerA 180
 Db 554 TAATATGCTGAACTCAAGGAAGGTCCTCCACTACAGTTGAACTGCGAC 613
 Qy 180 SASnGlnLysIleProThrLeuTriPheLeuAla-GluMetThrSerProValLeu 199
 Db 614 ACTCCCCGACATGCTTACGCCATGGCTGGCGCAATGAGCTCACAGTATATCGTG 673
 Qy 200 SASnAlaser-ThrGluTyrsThrGlySerCysThrValLeuLysAsnArgVal-G1 219
 Db 674 AAGAACGCCAGTTGAGTATCTGGACATACAGCTGCGACGGTCAAAACCGAGGG 733
 Qy 219 YserASP-GlnCysLeuLysLeuLysLeuAspValValProProSer 233
 Db 734 CTCTGAAACCGAGTGTATCTGGCAACTACAGCTGTCACCCACCCCTCC 777
 RESULT 11
 AL555497 AL555497 885 bp mRNA linear EST 16-FEB-2001
 DEFINITION LOCUS AL555497 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK008YP075
 prime, mRNA sequence.
 ACCESSION AL555497
 VERSION AL555497.1 GI:12897284
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS 1 (bases 1 to 885)
 TITLE Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization

JOURNAL		COMMENT	
Unpublished (2001)		Contact : Genoscope Genoscope - Centre National de Séquençage BP 191 91016 EVRY cedex - France Email: secrf@genoscope.cns.fr.	
FEATURES		Location/Qualifiers	
source		1. - 885	
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="CSODK008YP07"			
/clone_1ib="LT_NLU06_PL2"			
/tissue_type="placenta"			
/note="Vector: pCMVSPORT 6; site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850 USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"			
BASE COUNT	272	a	182
ORIGIN	182	c	190
g	9	t	237
gaps:	0	4 others	
US-09-899-634C-2 (1-261) x AL555497 (1-885)			
Qy			
47 PROGLYIaspGlyProLeuaspIleGluTrpPheLeuSerProAlaAspAsnGlyLys		66	
6 CCCGAAGAACCGAGGAAACCTGGACATGGAGCTGATATTCAACGAGTGATAATCGAAAG		65	
67 ValAspGlnValIleIleLeutyrSerGlyAspIleIleTyrAspAspTyrrGlnAsp		86	
66 GTCGATCAGTGATTATTATATTCTGGAGACAATTATGACTACTATCCAGAT		125	
87 LeuGlyGlyArgValHisPheThrSerAsnAspLeuLysSerGlyAspDalaSerIleAsn		106	
126 CTCGAAGCCGACTACATTTCAGGTATGATCTAAATCTGGATCATTAAT		185	
107 ValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCysLysValLysIysAlaPro		126	
186 GTRACGAATTACACTCACATATGGCACATATCAGTGGAAAGGAAAGCTCT		245	
127 GlyValIgLyAsnLysLysIleGlnLeuThrValIleLysProSerGlyThrAspCys		146	
246 GGCTGTGCAAATTAAGAAGATTCATCTGGTAGTCTGTGTAAGCTCTGGCGGAGTGT		305	
147 TyrValAspGlySerGluGluIleGlyAsnAspPheAspLysLysCysGluProLysGlu		166	
306 TAGTTGATGGATCTGAAGAAATTGGAACCAAAAGAA		365	
167 GlySerLeuProLeuLeuTyrglutrglnLysLeuSerAsnSerGlyIlysLeuProThr		186	
366 GGTTCACHTCCATTCAGTATGAGTGGCAAMATTGTTGACTCACAGAAATGCCACT		425	
187 LeuTrpIleuAlaGluMetThrSerProValleSerVallylsnAlaSerThrGlnLysTyr		206	
426 TCTGTGTTAGCAGAAAGTCACTCTGTTATCTGTTAAATGTAACCAAAAGAA		485	
207 SerGlyThrTyserCysThrVallylsnArgValGlySerAspGlnCysLeuLeuArg		226	
486 TCTGGACATACAGCTGTACAGTCAGACAGTGCTGCTCTGAGTCTGAGTAC		545	
227 LeuAspGlyValProProSerSerArgAlaGlyThrIleAlaGlyValleGlyVal		246	
BASE COUNT		206	
ORIGIN	206	a	155
g	9	c	151
gaps:	0	g	168
g	13	t	
US-09-899-634C-2 (1-261) x BM537136 (1-680)			
Qy			
1 MetalalauLeuLeuCysPheValleuLysGlyValAlaAspLeuThrArgSerLeu		20	
61 ATGGCGCTCTGCTGGCTTCTGCGGAGTCGGGATTCACCGAAAGTTG		120	
Qy			
21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyroLeuPro		40	
121 AGTATCACTACTCTGACAGATGATGAAAGGCCAAAGGGAAACTGCTTATTGCCA		180	
41 CysArgGlyIleGluGlyProGluAspGlyProLeuAspIleGluLeuLeuAsp		60	
181 TCCAATTTACCTTACTCCAGAGACGACGACGGCTGGTGGTGTCTCA		246	
Db	Qy	Qy	Qy
546 CTAACTTGTCTCTCTTCAATAAGCTGAGCTTAATGGAGGACCTATTAGGAACT	247 IleLeuAlaLeuValleuValleuGlyLeuLeuLeuPhcCysCysBarg	650	261
LOCUS	BM537136	LOCUS	BM537136
DEFINITION	ha78e07_91 Canis cDNAs from testes cells	DEFINITION	ha78e07_91 mRNA sequence.
VERSION	BM537136	VERSION	BM537136
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	Canis familiaris	SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;	ORGANISM	O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)	TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)
JOURNAL	Unpublished (2002)	JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie	COMMENT	Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center	Cold Spring Harbor Laboratory	Authors	Lita Annenberg Hazen Genome Sequencing Center
PO Box 100, Cold Spring Harbor, NY 11724, USA	PO Box 100, Cold Spring Harbor, NY 11724, USA	REFERENCE	McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
Plate: ha78	row: e	Plate: ha78	row: e
Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev
High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.
FEATURES	source	FEATURES	source
Alignment Scores:		1. - 680	
Pred. No. :		/organism="Canis familiaris"	
Score:		/db_xref="taxon:9606"	
Percent Similarity:		/clone="na78e07_91"	
Best Local Similarity:		/clone_1ib="Canis cDNAs from testes cells"	
Query Match:		/tissue_type="testes"	
DB:		/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using streptavidine zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."	
BASE COUNT		206	
ORIGIN	206	a	155
g	9	c	151
g	13	t	168
g	0	g	
Db	Qy	Qy	Qy
546 CTAACTTGTCTCTCTTCAATAAGCTGAGCTTAATGGAGGACCTATTAGGAACT	247 IleLeuAlaLeuValleuValleuGlyLeuLeuLeuPhcCysCysBarg	650	261
LOCUS	BM537136	LOCUS	BM537136
DEFINITION	ha78e07_91 Canis cDNAs from testes cells	DEFINITION	ha78e07_91 mRNA sequence.
VERSION	BM537136	VERSION	BM537136
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	Canis familiaris	SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;	ORGANISM	O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)	TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)
JOURNAL	Unpublished (2002)	JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie	COMMENT	Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center	Cold Spring Harbor Laboratory	Authors	Lita Annenberg Hazen Genome Sequencing Center
PO Box 100, Cold Spring Harbor, NY 11724, USA	PO Box 100, Cold Spring Harbor, NY 11724, USA	REFERENCE	McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
Plate: ha78	row: e	Plate: ha78	row: e
Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev
High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.
FEATURES	source	FEATURES	source
Alignment Scores:		1. - 680	
Pred. No. :		/organism="Canis familiaris"	
Score:		/db_xref="taxon:9606"	
Percent Similarity:		/clone="na78e07_91"	
Best Local Similarity:		/clone_1ib="Canis cDNAs from testes cells"	
Query Match:		/tissue_type="testes"	
DB:		/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using streptavidine zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."	
BASE COUNT		206	
ORIGIN	206	a	155
g	9	c	151
g	13	t	168
g	0	g	
Db	Qy	Qy	Qy
546 CTAACTTGTCTCTCTTCAATAAGCTGAGCTTAATGGAGGACCTATTAGGAACT	247 IleLeuAlaLeuValleuValleuGlyLeuLeuLeuPhcCysCysBarg	650	261
LOCUS	BM537136	LOCUS	BM537136
DEFINITION	ha78e07_91 Canis cDNAs from testes cells	DEFINITION	ha78e07_91 mRNA sequence.
VERSION	BM537136	VERSION	BM537136
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	Canis familiaris	SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;	ORGANISM	O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)	TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)
JOURNAL	Unpublished (2002)	JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie	COMMENT	Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center	Cold Spring Harbor Laboratory	Authors	Lita Annenberg Hazen Genome Sequencing Center
PO Box 100, Cold Spring Harbor, NY 11724, USA	PO Box 100, Cold Spring Harbor, NY 11724, USA	REFERENCE	McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
Plate: ha78	row: e	Plate: ha78	row: e
Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev
High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.
FEATURES	source	FEATURES	source
Alignment Scores:		1. - 680	
Pred. No. :		/organism="Canis familiaris"	
Score:		/db_xref="taxon:9606"	
Percent Similarity:		/clone="na78e07_91"	
Best Local Similarity:		/clone_1ib="Canis cDNAs from testes cells"	
Query Match:		/tissue_type="testes"	
DB:		/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using streptavidine zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."	
BASE COUNT		206	
ORIGIN	206	a	155
g	9	c	151
g	13	t	168
g	0	g	
Db	Qy	Qy	Qy
546 CTAACTTGTCTCTCTTCAATAAGCTGAGCTTAATGGAGGACCTATTAGGAACT	247 IleLeuAlaLeuValleuValleuGlyLeuLeuLeuPhcCysCysBarg	650	261
LOCUS	BM537136	LOCUS	BM537136
DEFINITION	ha78e07_91 Canis cDNAs from testes cells	DEFINITION	ha78e07_91 mRNA sequence.
VERSION	BM537136	VERSION	BM537136
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	Canis familiaris	SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;	ORGANISM	O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)	TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)
JOURNAL	Unpublished (2002)	JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie	COMMENT	Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center	Cold Spring Harbor Laboratory	Authors	Lita Annenberg Hazen Genome Sequencing Center
PO Box 100, Cold Spring Harbor, NY 11724, USA	PO Box 100, Cold Spring Harbor, NY 11724, USA	REFERENCE	McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
Plate: ha78	row: e	Plate: ha78	row: e
Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev
High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.
FEATURES	source	FEATURES	source
Alignment Scores:		1. - 680	
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Score:		/db_xref="taxon:9606"	
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Best Local Similarity:		/clone_1ib="Canis cDNAs from testes cells"	
Query Match:		/tissue_type="testes"	
DB:		/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using streptavidine zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."	
BASE COUNT		206	
ORIGIN	206	a	155
g	9	c	151
g	13	t	168
g	0	g	
Db	Qy	Qy	Qy
546 CTAACTTGTCTCTCTTCAATAAGCTGAGCTTAATGGAGGACCTATTAGGAACT	247 IleLeuAlaLeuValleuValleuGlyLeuLeuLeuPhcCysCysBarg	650	261
LOCUS	BM537136	LOCUS	BM537136
DEFINITION	ha78e07_91 Canis cDNAs from testes cells	DEFINITION	ha78e07_91 mRNA sequence.
VERSION	BM537136	VERSION	BM537136
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	Canis familiaris	SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;	ORGANISM	O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)	TITLE	Expressed sequence tags from Canis familiaris (dog) (2002)
JOURNAL	Unpublished (2002)	JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie	COMMENT	Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center	Cold Spring Harbor Laboratory	Authors	Lita Annenberg Hazen Genome Sequencing Center
PO Box 100, Cold Spring Harbor, NY 11724, USA	PO Box 100, Cold Spring Harbor, NY 11724, USA	REFERENCE	McCombie,W.R., Baker,J.P., Balija,V., Cunnus,M., D., Dedhia,N., de la Basile,M., Katzenberger,F., King,L., Kirchoff,D.N., Miller,B., Muller,S., Nascentio,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Preston,R. and Hannon,G.J.
Plate: ha78	row: e	Plate: ha78	row: e
Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev	Seq primer: -21M1uni+rev
High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.	High quality sequence stop: 680.
FEATURES	source	FEATURES	source
Alignment Scores:		1. - 680	
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Percent Similarity:		/clone="na78e07_91"	
Best Local Similarity:		/clone_1ib="Canis cDNAs from testes cells"	
Query Match:		/tissue_type="testes"	
DB:		/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using streptavidine zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."	
BASE COUNT		206	
ORIGIN	206	a	155
g	9	c	151
g	13	t	168
g	0	g	
Db	Qy	Qy	Qy
546 CTAACTTGTCTCTCTTCAATAAGCTGAGCTTAATGGAGGACCTATTAGGAACT	247 IleLeuAlaLeuValleuValleuGlyLeuLeuLeuPhcCysCysBarg	650	261
LOCUS	BM537136	LOCUS	BM537136
DEFINITION			

insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."

	BASE COUNT	ORIGIN
Qy 61 ProAlaAspAsnGlnIysValAspGlnValLeuThrSerGlyAspLysLeuYr 80	241 CCAGCTGATAATCAGAAAGTGACGATATTATCTGGAGACAATTAT 300	
Qy 81 AspAspTYrTyrgInAspLeuIysGlyArgValHisPheThrSerAspAspLeuLysSer 100	301 GACGACTACTATCAGACCTGAGAGACGATCAATTACAGCAATGCTCAAATCT 360	
Qy 101 GlyAspAlaSerIleAsnValThrAspLeuGlnLeuAspIleGlyAspLysLeu 120	361 GGTCATGTGATCCATAAATCTAACCAATTACGGTTGCAAGATTTGGCACTACAGTC 420	
Qy 121 LysValLysLysAlaProGlyValGlyAsnLysIleGlnLeuThrValLeuLys 140	421 AAAGTGAAGAAAGCTCCTGGTGGAAATAAGAGATTCAGTGACAGTCTGTGTA 480	
Qy 141 ProSerGlyThrArgCysTyrvAlAspGlySerGluGluIleGlyAsnAspPhenylSleu 160	481 CCTCAGGTTAAGTGTGATGTCAGAGAAATGCTTA 540	
Qy 161 LysCysGluProLygGlyIysSerIleAspLeuProLeuLeuThrGluTrpGlyLysLeu 180	541 AAATGTCGACCAAAAGAGCTTCACTTCATCAATGAAATGCAAAATGTCAT 600	
Qy 181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValIys 200	601 TCACAGAAAACGCCCGCCCTGCTGTCAGATATGACTCTACCTGTATCTATAAA 660	
Qy 201 AsnAlaSerThrGluYr 206	651 AATGCCCTCATGTGATC 678	
Db RESULT 13		
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LOCUS B1823597		
REFERENCE 1 B1823597		
VERSION B1823597.1		
KEYWORDS EST.		
SOURCE		
ORGANISM		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 885)		
AUTHORS NIH-MGC http://mgc.nci.nih.gov/		
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL Unpublished (1999)		
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov		
Tissue Procurement: Life Technologies, Inc.		
CDNA Library Preparation: Life Technologies, Inc.		
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIINL)		
DNA Sequencing by: Incyte Genomics, Inc.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIINL at: http://image.llnl.gov/Plate: LIIM1453 Row: j column: 16		
High quality sequence stop: 705.		
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source		
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/db_xref="Taxon:9606"		
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/clone.lib="NIH_MGC_115"		
/lab.host="DHB10"		
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Qy 1 219 Gly-----SerAspGlnCys--LeuLeuArgLeuAspValValProProSer 233		
Db 735 GGAGCTCATGACTCCAGTGACAGTGGGTCAAAGGTTGTCGCCCTT-----TCA 788		
Qy 234 Asn-Arg-Ala-Gly-Ythr-Ile-Ala-Gly-Yala-Valle-Gly-Valle-Ule-Ula 249		
Db 789 AACAAAGCTGGACTAATTCGAGGAGCTTAAAGACTTGCTGGCA 837		
DEFINITION 602874325P1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006094 5',	RESULT 14	
LOCUS B1077977 B1077977 702 bp mRNA linear EST 20-JUN-2001		

			mRNA sequence.
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VERSION	B1077977.1	GI:14496307	B1077977.1
KEYWORDS	EST.	Db	430 AAGTGAGAAAGCCCTGGGTCGGACATAAGAATTCTGTGACCGTCTGTGTAAG 489
SOURCE	house mouse.	QY	141 ProSerGlyThrArgCysTyrValAspGlySer--GluGluLeuGlyAsn-AspPhe 159
ORGANISM	Mus musculus	Db	141 ProSerGlyThrArgCysTyrValAspGlySer--GluGluLeuGlyAsn-AspPhe 159
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus. (bases 1 to 702)	QY	159 SerLysCysGluProLysGluGlySerIleProLeuLeuTyGluTrpGlnLysLeu 179
REFERENCE	NIM-MGC http://mgc.nci.nih.gov/	Db	159 SerLysCysGluProLysGluGlySerIleProLeuLeuTyGluTrpGlnLysLeu 179
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	QY	550 GCTAAATGAGAACCCAAAGGAACGCTCTTCACTACAGTTGATGGCAGAACGTC 609
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgaphs@mail.nih.gov	Db	550 GCTAAATGAGAACCCAAAGGAACGCTCTTCACTACAGTTGATGGCAGAACGTC 609
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	QY	179 RasnSerGlnLysLeuProThrLeuPheLeuAlaGluMetThrSerProValLeuSerVa 199
Plate: LIAM11047 row: a column: 07	High quality sequence stop: 700.	Db	179 RasnSerGlnLysLeuProThrLeuPheLeuAlaGluMetThrSerProValLeuSerVa 199
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	/tissue type="tumor, biopsy sample"	DEFINITION	AL514786 LTI_NFL006_PL2 Homo sapiens mRNA linear EST 13_FEB-2001
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	/lab_host="DPL10B"	VERSION	AL514786.1 GI:12778279
	/note="Organ: mammary; Vector: pCMW-SPORT6; Site 1: SALL; Site 2: NotI; Cloned unidirectionally; Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"	AUTHORS	Li, W.B., Gruber, C.S., Jesse, J. and Polayes, D.
	BASE COUNT	JOURNAL	Full-length cDNA libraries and normalization
ORIGIN	197 a 172 c 173 g 160 t	COMMENT	Unpublished (2001)
Alignment Scores:	Pred. No.: 2.05e-93	FEATURES	ORGANISM
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Query Match:	Mismatches: 85.31%		AL514786
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			human.
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QY	21 SerIleThrThrProGluGlnMetIleGluLysAlaGlyGluThraIaTyruLeuPro 40		
Db	131 AGCATCACTACACCCGAACTGAGGATCGAAAGGGAACTGGTATCTCA 190		
QY	41 CysArgPheThrLeuGlyProGluLysPheGlyProLeuAspPheGluLeuSer 60		
Db	191 TGCAGTTTACTCTCAGTCCGAAGACCA-GGACCACTGACATGAGTCGATATCC 249		
QY	61 ProAlaAspIasnGlnLysValAspGlnValAlaIleLeuTyrSerGlyAspLysLeuTyr 80	Alignment Scores:	
Db	250 CGCTGTGATACCAAGATAGTAGGATGATCATTGATTCGGAGCAAAATT 309	Pred. No.: 7.87e-93	
QY	81 AspAspPtyrGlyGlnAspIleuLysGlyAspValHisPheThrSerAsnAspLeuSer 100	Length: 838	
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QY	101 GlyAlaPheSerIleAsnValThrAsnLeuGlnIleSerAspPheGlyThrTyrglnCys 120	Matches: 180	
Db	370 GGCAGACGCACTATAATGtgACCACCTCAGCTGCTGCACTTACCACTG 429	Conservative: 14	
		Mismatches: 30	
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		Gaps: 2	
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Db 67 ATGGCGCTCTGCGTGCCTCGCTCGAGTAGTGGATTCCGCAAGTTG 126
 Qy 21 SerIleThrProGluLmMetIleGluLysAlaGlyGlutnAlaIleLeuPro 40
 Db 127 AGFATCACTACTCTGAAGAGCATGAAAGCCAAAGGGAACTGCCATCTGCCA 186
 Qy 41 CysArgPheIleIeuGlyProGluAspGlnGlyProLeuAspIleGluIleLeuSer 60
 Db 187 TGCACATTACGCTAGCAGCCGAGCAGGAGCTGGACATCGAGGCTGATACA 246
 Qy 61 ProLysAspAspGlnLysValAspGlnValIleIleLeuTyserGlyAspIleTyr 80
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 Qy 181 SerGlnIlysIleProThrIleTrpLeuAla--GluMetThrSerProValIleSerVal 199
 Db 607 TCACAGAAATGCCACTTCATGGTTAGCAGGGAGATGTG-CCACCTCCAAAGGCCGT 665
 Qy 200 LysAsnIlaSerThrGluItySerGlyThrTySerCysThrValIleAsnArgValGly 219
 Db 666 ACGTCCACTGCCAGAAGCTACATGGCAGTTATCATTATCC----- 707
 Qy 220 SerAspGlnCysLeuLeuArgIleAspValValProProSerIleArgAlaGly 237
 Db 708 -----CTGGGTCATGTCCTCCATCATGGAGGA 740

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